

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:06:38 ; Search time 3.38828 Seconds
(without alignments)
1250.845 Million cell updates/sec

Title: US-09-785-215-4
Perfect score: 74
Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query Match Length DB	ID	Description
	Score				
1	74	100.0	15 2	AAR06310	Aar06310 Tetanus t
2	74	100.0	15 2	ADB87354	Adb87354 Cytotoxic
3	74	100.0	15 2	AAW11505	Aaw11505 Tetanus t
4	74	100.0	15 2	AAW35506	Aaw35506 Universal
5	74	100.0	15 2	AAW71321	Aaw71321 Universal
6	74	100.0	15 2	AAW67033	Aaw67033 Tetanus t
7	74	100.0	15 2	AAW67578	Aaw67578 T-cell ep
8	74	100.0	15 2	AAY04051	Aay04051 T-Helper
9	74	100.0	15 2	AAW73220	Aaw73220 Tetanus t

10	74	100.0	15	3	AAAY92625	Aay92625 Foreign e
11	74	100.0	15	3	AAAY70300	Aay70300 Clostridi
12	74	100.0	15	3	AAAY84427	Aay84427 Amino aci
13	74	100.0	15	3	AAAY82637	Aay82637 Tetanus t
14	74	100.0	15	3	AAAY44763	Aay44763 Tetanus t
15	74	100.0	15	3	AAB45511	Aab45511 Tetanus P
16	74	100.0	15	4	AAE11763	Aae11763 Clostridi
17	74	100.0	15	4	AAB49071	Aab49071 Tetanus t
18	74	100.0	15	4	AAM99515	Aam99515 Vaccine r
19	74	100.0	15	4	AAB46172	Aab46172 Tetanus t
20	74	100.0	15	4	AAB68636	Aab68636 HER-2 B c
21	74	100.0	15	4	AAB61956	Aab61956 Tetanus T
22	74	100.0	15	4	AAB20143	Aab20143 Tetanus t
23	74	100.0	15	4	AAB85451	Aab85451 Wild-type
24	74	100.0	15	4	AAB85701	Aab85701 Amino aci
25	74	100.0	15	5	AAU97872	Aau97872 Tetanus t
26	74	100.0	15	5	ABG31774	Abg31774 T helper
27	74	100.0	15	6	ABG72721	Abg72721 Tetanus t
28	74	100.0	15	6	ABP72694	Abp72694 Tetanus t
29	74	100.0	15	6	ADA25169	Ada25169 C. tetani
30	74	100.0	15	6	AAO30454	Aao30454 Tetanus t
31	74	100.0	15	7	ABR82482	Abr82482 Tetanus t
32	74	100.0	15	7	ADC09976	Adc09976 Tetanus t
33	74	100.0	15	7	ADC89658	Adc89658 C. tetani
34	74	100.0	15	7	ADC81609	Adc81609 Tetanus t
35	74	100.0	16	2	AAW35445	Aaw35445 T-cell st
36	74	100.0	16	2	AAAY29705	Aay29705 Clostridi
37	74	100.0	16	5	AAU11413	Aau11413 Tetanus t
38	74	100.0	16	5	AAU93865	Aau93865 Clostridi
39	74	100.0	16	7	ADE10941	Adel0941 Chimeric
40	74	100.0	17	2	AAR62692	Aar62692 Helper T
41	74	100.0	17	2	AAR82573	Aar82573 Tetanus t
42	74	100.0	17	2	AAR88395	Aar88395 T-cell an
43	74	100.0	17	2	AAW05599	Aaw05599 Tetanus t
44	74	100.0	17	3	AAAY99274	Aay99274 HLA class
45	74	100.0	17	3	AAAY58768	Aay58768 Unidentif

ALIGNMENTS

RESULT 1

AAR06310

ID AAR06310 standard; protein; 15 AA.

XX

AC AAR06310;

XX

DT 04-DEC-1990 (first entry)

XX

DE Tetanus toxin epitope.

XX

KW Tetanus toxin; vaccine; major histocompatibility complex; MHC;

KW antimalarial.

XX

OS Synthetic.

XX

PN EP378881-A.

XX
PD 25-JUL-1990.
XX
PF 27-DEC-1989; 89EP-00203318.
XX
PR 17-JAN-1989; 89IT-00019110.
PR 16-NOV-1989; 89IT-00022409.
XX
PA (ENIE) ENIRICERCHE SPA.
XX
PI Pessi A, Bianchi E, Verdini AS, Corradin G;
XX
DR WPI; 1990-225582/30.
XX
PT Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used as
PT universal carriers for prepn. of immunogenic conjugate(s) for use as
PT vaccines.
XX
PS Claim 1; Page 17; 20pp; English.
XX
CC Epitopic peptides may be used with synthetic hapten derived from a
CC pathogen to generate an immune response to the pathogen. Peptides are
CC recognised by numerous T-helper cell clones within the context of a wide
CC range of alleles of the human MHC. The peptides may be used in an
CC antimalarial vaccine inducing Ab. response to P.falciparum
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 2

ADB87354

ID ADB87354 standard; peptide; 15 AA.

XX

AC ADB87354;

XX

DT 04-DEC-2003 (first entry)

XX

DE Cytotoxic T epitope retro-partly inverso peptide TT830-844.

XX

KW immunoretroid; anti-immunoretroid; CONH linkage; NHCO linkage;

KW retropeptide; retroinverse peptide; vaccine; viral; bacterial infection;

KW autoimmune disease; neurodegenerative disease; retro-partly;

KW inverso peptide.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Modified by H"

FT Modified-site 15
 FT /note= "Modified by OH"
 XX
 PN FR2717081-A1.
 XX
 PD 15-SEP-1995.
 XX
 PF 14-MAR-1994; 94FR-00002950.
 XX
 PR 14-MAR-1994; 94FR-00002950.
 XX
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Guichard G, Muller S, Briand J, Regenmortel MHV;
 XX
 DR WPI; 1995-322414/42.
 XX
 PT Therapeutic and diagnostic uses of retro peptide analogues - corresp. to
 PT parent peptide chains with CONH linkages replaced by NHCO linkages, also
 PT antibodies against the peptide(s).
 XX
 PS Disclosure; Page 22; 58pp; French.
 XX
 CC This invention relates to the novel uses of 'immunoretroids' or anti-
 CC immunoretroid antibodies, where the immunoretroids are peptide analogues
 CC in which one or more (preferably all) of the CONH linkages in the chain
 CC of the corresponding parent peptides are replaced by NHCO linkages and
 CC the chirality of each amino acid residue, whether involved in NHCO
 CC linkages or not, is either conserved or inverted with regards to the
 CC corresponding amino acid residue in the parent peptides. For example,
 CC 'retropeptides' or 'retroinverse peptides', provided that the
 CC immunoretroids are capable of forming complexes with the anti-
 CC immunoretroid antibodies and with antibodies directed against the parent
 CC peptides or parent proteins and/or the parent peptide enantiomers or
 CC parent protein enantiomers. The immunoretroids are used to prepare
 CC medicaments for preventing or treating pathologies associated with the
 CC presence of an exogenous or endogenous protein capable of being
 CC implicated directly or indirectly in the appearance and/or development of
 CC the pathologies. Immunoretroids can also be used to prepare vaccines for
 CC preventing pathologies associated with the presence of an exogenous or
 CC endogenous protein recognised by antibodies directed against
 CC immunoretroids. Comparisons containing immunoretroids associated with a
 CC carrier molecule capable of inducing production of antibodies against an
 CC exogenous or endogenous protein responsible for a pathology, or of
 CC inducing a cytotoxic cellular immune response are useful as vaccines.
 CC Pathologies that can be diagnosed or treated are especially viral or
 CC bacterial infections, autoimmune diseases and neurodegenerative diseases.
 CC This sequence represents a cytotoxic T epitope related retro-partly
 CC inverso peptide relating to the retropeptides of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

Db

|||||||
1 QYIKANSKFIGITEL 15

RESULT 3

AAW11505

ID AAW11505 standard; protein; 15 AA.

XX

AC AAW11505;

XX

DT 24-SEP-1997 (first entry)

XX

DE Tetanus toxoid universal Th epitope TT830.

XX

KW Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;

KW fusion protein; chimera; tetanus toxoid; helper T cell epitope;

KW antigen presentation; ds.

XX

OS Clostridium tetani.

XX

PN WO9640789-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009988.

XX

PR 07-JUN-1995; 95US-00484172.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Deo YM, Goldstein J, Graziano R, Somasundaram C;

XX

DR WPI; 1997-052242/05.

DR N-PSDB; AAT58127.

XX

PT Recombinant, multi-specific anti-Fc receptor antibody molecules - also

PT comprise an anti-target portion, used for the treatment of cancer,

PT autoimmune disease and pathogenic infection.

XX

PS Example 7; Fig 24; 115pp; English.

XX

CC Synthetic DNA coding for the wild-type universal Th epitope from tetanus

CC toxoid, designated TT830, was fused to the 3'-end of DNA encoding heavy

CC chain sequences from the humanised anti-Fc gamma RI monoclonal antibody

CC H22. The resulting fusion protein was shown to be significantly more

CC efficient in antigen presentation and T cell stimulation than the TT830

CC epitope alone. A similar fusion construct was prepared coding for a

CC mutant, antagonistic form of the epitope (designated TT833S) fused to the

CC anti-Fc gamma RI. The Fab22-TT833S is at least 100 times more effective

CC than TT833S in inhibiting T cell activation

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 7.5e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
 |||||||
Db 1 QYIKANSKFIGITEL 15

RESULT 4

AAW35506

ID AAW35506 standard; peptide; 15 AA.

XX

AC AAW35506;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1998 (first entry)

XX

DE Universal T-cell epitope peptide SEQ ID NO:8.

XX

KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;

KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX

OS Unidentified.

XX

PN W09738011-A1.

XX

PD 16-OCT-1997.

XX

PF 03-APR-1997; 97WO-DK000146.

XX

PR 03-APR-1996; 96DK-00000398.

XX

PA (PEPR-) PEPRESEARCH AS.

XX

PI Heegaard PMH, Jakobsen PH;

XX

DR WPI; 1997-512645/47.

XX

PT Non-dendritic peptide carrier linked to a solid phase - useful as a

PT diagnostic agent and as a scaffold for production of chemical

PT derivatives.

XX

PS Example 20; Page 124; 262pp; English.

XX

CC A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence represents
CC a peptide used in an example from the present invention. An (A)-solid
CC phase complex can be used as a scaffold for the production of chemical
CC derivatives, characterised by covalently attaching molecules at
CC attachment points. Alternatively (A) is used as a scaffold-peptide for
CC the incorporation into an Immunostimulating Complex (Iscom) resulting an
CC (A)-Iscom complex which is used for the chemical coupling of antigenic
CC substances in an aqueous solution by conjugation. (A) derivatised with
CC one or more peptides having fibronectin-, laminin- or vitronectin-like
CC binding activities can be used for the promotion of cell-attachment to
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,

CC and for promotion of wound healing. Also a derivatised (A) can be used
CC for the selection of specifically-binding aptamers or as a diagnostic
CC agent. Such diagnostic-(A) molecules could be used to detect molecules
CC derived from or indicative of pregnancy or of a disease, such as an
CC infectious, autoimmune or cancerous disease. (Updated on 25-MAR-2003 to
CC correct PF field.)

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 5

AAW71321

ID AAW71321 standard; peptide; 15 AA.

XX

AC AAW71321;

XX

DT 26-NOV-1998 (first entry)

XX

DE Universal helper T-cell epitope P2 derived from tetanus toxin.

XX

KW Liver stage; Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3;

KW hepatic and erythrocytic stage protein; PyHEP17; vaccine;

KW malaria parasite; tetanus toxin; P2; helper T-cell epitope.

XX

OS Synthetic.

OS Clostridium tetani.

XX

PN US5814617-A.

XX

PD 29-SEP-1998.

XX

PF 07-OCT-1994; 94US-00319704.

XX

PR 07-OCT-1994; 94US-00319704.

XX

PA (USNA) US SEC OF NAVY.

XX

PI Doolan DL, Charoenvit Y, Hoffman SL, Hedstrom RC;

XX

DR WPI; 1998-541794/46.

XX

PT Vaccine for protecting mammal against infection by malaria caused by

PT Plasmodium species - comprises a first nucleic acid encoding a first

PT polypeptide capable of eliciting an immune reaction against an antigen

PT expressed during the liver.

XX

PS Disclosure; Col 12; 24pp; English.

XX

CC AAW71321-22 represent universal helper T-cell epitopes derived from

CC tetanus toxin. They are used to enhance host immune response to vaccines.
CC The specification describes a Plasmodium yoelii liver stage 17 kDa
CC hepatic and erythrocytic stage protein designated PyHEP17. This protein
CC elicits a response from an Ig1 monoclonal antibody designated Navy Yoelii
CC Liver Stage 3 (NYLS3). This antibody does not recognise sporozoites, but
CC does recognise P. yoelii liver stage parasites. NYLS3 eliminates upto 90%
CC of liver stage parasites. The specification describes a vaccine for
CC reducing the severity or incidence of infection by a malaria parasite of
CC the genus Plasmodium. The DNA vaccine comprises exon 1 and part of exon 2
CC of the PyHEP17 gene

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

|||||||

Db 1 QYIKANSKFIGITEL 15

RESULT 6

AAW67033

ID AAW67033 standard; peptide; 15 AA.

XX

AC AAW67033;

XX

DT 15-DEC-1998 (first entry)

XX

DE Tetanus toxin fragment (residues 830-844).

XX

KW Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate;

KW dendrimeric poly-lysine; epitope; tumour.

XX

OS Clostridium tetani.

XX

PN W09843677-A1.

XX

PD 08-OCT-1998.

XX

PF 27-MAR-1998; 98WO-EP001922.

XX

PR 27-MAR-1997; 97US-0041726P.

XX

PA (INSP) INST PASTEUR.

XX

PI Bay S, Cantacuzene D, Leclerc C, Lo-Man R;

XX

DR WPI; 1998-557071/47.

XX

PT Carbohydrate peptide conjugate used as vaccine - comprises carrier with

PT dendrimeric poly-lysine enabling multiple epitopes to be covalently

PT attached.

XX

PS Disclosure; Page 13; 55pp; English.

XX

CC The invention relates to a new carbohydrate peptide conjugate, which
 CC comprises a carrier with a dendrimeric poly-lysine enabling multiple
 CC epitopes to be covalently attached to it. Also claimed are: (1) an
 CC antibody purified from biological fluid or cells of organisms
 CC administered with the carbohydrate peptide conjugate, and (2) a diagnosis
 CC kit comprising antigen-specific antibodies elicited by immunisation with
 CC the carbohydrate peptide conjugate. The peptide conjugate, antibody and
 CC diagnosis kit are used to provide pharmaceutical compositions and
 CC vaccines against tumours. These can be used to support an immune response
 CC against viral infections caused by hepatitis virus, HIV or cytomegalo
 CC virus. They can be used to enhance immune responses, especially B- and T-
 CC cell responses, of humans and animals against bacterial infections. The
 CC carbohydrate peptide conjugate stimulates the antibody and T-cell
 CC response without stimulating undesired immune responses. The composition
 CC is capable of increasing the survival of tumour bearing humans and
 CC animals. The present sequence corresponds to residues 830-844 of tetanus
 CC toxin. The synthetic peptide corresponding to this sequence may be used
 CC as an epitope in a carbohydrate peptide conjugate

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

RESULT 7

AAW67578

ID AAW67578 standard; peptide; 15 AA.

XX

AC AAW67578;

XX

DT 02-MAR-1999 (first entry)

XX

DE T-cell epitope peptide #4 for chimeric fimbrin/T-cell epitope peptide.

XX

KW Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
 KW immunogenic composition; immune response.

XX

OS Synthetic.

XX

PN US5843464-A.

XX

PD 01-DEC-1998.

XX

PF 02-JUN-1995; 95US-00460502.

XX

PR 02-JUN-1995; 95US-00460502.

XX

PA (OHIS) UNIV OHIO STATE.

XX

PI Kaumaya PTP, Bakaletz LO;

XX

DR WPI; 1999-044514/04.
 XX
 PT Synthetic chimeric fimbrin peptide - useful for vaccination against non-
 PT typable Haemophilus influenzae.
 XX
 PS Disclosure; Col 4; 16pp; English.
 XX
 CC The invention relates to the manufacture of a synthetic chimeric peptide
 CC comprising a non-typable Haemophilus influenzae fimbrin peptide fused via
 CC a linker peptide to a T-cell epitope peptide. The chimeric peptide is
 CC used in immunogenic compositions which induce an immune response against
 CC non-typable Haemophilus influenzae. This sequence represents an example
 CC of a T-cell epitope peptide used to generate the chimeric peptide
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

RESULT 8

AAY04051

ID AAY04051 standard; peptide; 15 AA.

XX

AC AAY04051;

XX

DT 04-JAN-2000 (first entry)

XX

DE T-Helper epitope from tetanus toxoid.

XX

KW Covalently reactive antigen analog; CRAA; catalytic antibody;

KW electrophilic reaction centre; phosphonate; boronate; vaccine;

KW transition state analog; TSA; isostere; gp120; HIV-1; T-helper; tetanus;

KW toxoid; B-T-epitope.

XX

OS Clostridium tetani.

XX

PN WO9948925-A1.

XX

PD 30-SEP-1999.

XX

PF 23-MAR-1999; 99WO-US006325.

XX

PR 23-MAR-1998; 98US-00046373.

XX

PA (UYNE-) UNIV NEBRASKA.

XX

PI Paul S, Gololobov G, Smith L;

XX

DR WPI; 1999-591076/50.

XX

PT New covalently reactive antigen analogs used for treating e.g. autoimmune

PT diseases, lymphoproliferative disorders, cancers, microbial infections,
PT ischemic and reperfusion injury or septic shock.
XX
PS Disclosure; Page 86; 158pp; English.
XX
CC The patent discloses new covalently reactive antigen analogs (CRAA) of
CC formula X1-Y-E-X2, in which X1 and X2 represent peptide sequences of an
CC epitope of a disease-associated protein, Y is a positively charged amino
CC acid residue, preferably Lys or Arg, and E is an electrophilic reaction
CC centre, preferably a phosphonate or boronate moiety. Depending on the
CC identity of the epitope, the CRAA may be used to stimulate production of
CC catalytic antibodies specific for predetermined antigens associated with
CC particular medical disorders. They may also be used to permanently
CC inactivate endogenously produced catalytic antibodies produced in certain
CC autoimmune diseases as well as in certain lymphoproliferative disorders.
CC Amongst the specifically exemplified CRAAs is one based on residues 421-
CC 436 of a B-cell epitope of gp120 (see AAY04046) which may be used to
CC counter HIV-1 infections. When used as an immunogen, preferably this CRAA
CC is conjugated at its N-terminal to a T-helper epitope from tetanus
CC toxoid. The present sequence represents the T-helper epitope and
CC corresponds to residues 830-844 of the toxoid
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
|||||||
Db 1 QYIKANSKFIGITEL 15

RESULT 9

AAW73220

ID AAW73220 standard; protein; 15 AA.

XX

AC AAW73220;

XX

DT 25-JAN-1999 (first entry)

XX

DE Tetanus toxoid epitope.

XX

KW Multispecific single chain antibody; antibody H22; tumour cell; therapy;
KW antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
KW epidermal growth factor receptor; breast cancer; ovarian cancer.

XX

OS Synthetic.

XX

PN US5837243-A.

XX

PD 17-NOV-1998.

XX

PF 07-JUN-1996; 96US-00661052.

XX

PR 07-JUN-1995; 95US-00484172.

XX

PA (MEDA-) MEDAREX INC.
 XX
 PI Somasundaram C, Graziano R, Deo YM, Goldstein J;
 XX
 DR WPI; 1999-023374/02.
 XX
 PT Specific killing of tumour cells - using a multi-specific molecule
 PT comprising an anti-Fc receptor antibody and a portion which binds to a
 PT target cell.
 XX
 PS Example 7; Col 27; 57pp; English.
 XX
 CC This sequence represents a tetanus toxoid epitope and is recognised by
 CC the multispecific single chain antibody designated H22. The antibody can
 CC be used in the method of the invention for inducing antibody-dependent
 CC cellular cytotoxicity (ADCC) against a tumour cell which is characterised
 CC by overexpression of HER 2/neu or epidermal growth factor receptor
 CC (EGFR), comprises contacting the tumour cell with a multispecific protein
 CC molecule (preferably a single chain antibody) comprising: (a) an anti-Fc
 CC receptor antibody or an antigen binding fragment; (b) a portion which
 CC binds to HER 2/neu; and (c) a portion which binds to EGFR. The method can
 CC be used for treating cancers especially breast cancer or ovarian cancer.
 CC The multispecific antibody can also be administered prophylactically to
 CC vaccinate a subject against infection by a target cell
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

RESULT 10

AAY92625

ID AAY92625 standard; protein; 15 AA.

XX

AC AAY92625;

XX

DT 10-AUG-2000 (first entry)

XX

DE Foreign epitope P2.

XX

KW Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2;

KW Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination;

KW cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;

KW prostate cancer; cell-associated peptide antigen.

XX

OS Clostridium tetani.

XX

PN WO200020027-A2.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-DK000525.
 XX
 PR 05-OCT-1998; 98DK-00001261.
 PR 20-OCT-1998; 98US-0105011P.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
 PI Gautam A, Birk P, Karlsson G;
 XX
 DR WPI; 2000-349917/30.
 DR N-PSDB; AAA09460.
 XX
 PT Inducing immune responses to weakly immunogenic, tumor associated peptide
 PT antigens for the treatment of breast and prostate cancer.
 XX
 PS Example 1; Page 213; 220pp; English.
 XX
 CC The claims detail a method for inducing immune responses against weakly
 CC immunogenic cell-associated peptide antigens (PA) such as those
 CC associated with cancers (i.e. self-proteins), for example, human prostate
 CC specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast
 CC growth factor 8b (FGF8b). The method comprises effecting simultaneous
 CC presentation by antigen producing cells (APCs) of the animals immune
 CC system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from
 CC the PA and/or at least 1 B-cell group derived from the cell-associated PA
 CC ; and (2) at least 1 first T helper cell group which is foreign to the
 CC animal. Analogues of human PSM, human Her2 and human/murine FGF8b
 CC comprising a substantial part of all known and predicted CTL and B-cell
 CC epitopes of the respective PA and including at least one foreign T helper
 CC epitope (e.g. P2 and/or P30) are also claimed. The method is used to
 CC treat prostate, prostate/breast or breast cancer when the PA is human
 CC PSM, FGF8b and Her2, respectively
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

RESULT 11

AAY70300

ID AAY70300 standard; peptide; 15 AA.

XX

AC AAY70300;

XX

DT 06-JUN-2000 (first entry)

XX

DE Clostridium tetani tetanus toxoid T-cell epitope, P589.

XX

KW Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;

KW T-cell epitope; tetanus toxoid; antigenic epitope; treatment;

KW circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;
 KW liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2;
 KW apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
 KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
 KW Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
 XX
 OS Clostridium tetani.
 XX
 PN WO200011179-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 19-AUG-1999; 99WO-US018869.
 XX
 PR 21-AUG-1998; 98US-0097703P.
 XX
 PA (NAIM-) NAT INST IMMUNOLOGY.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lal AA, Shi YP, Hasnain SE;
 XX
 DR WPI; 2000-237654/20.
 XX
 PT Novel recombinant protein as vaccine for treating malarial infection
 PT comprises antigenic peptides obtained from different stages of plasmodium
 PT falciparum life cycle.
 XX
 PS Claim 2; Page 17; 52pp; English.
 XX
 CC The present sequence is the tetanus toxoid T-cell epitope P589, derived
 CC from Clostridium tetani. It is used in the construction of recombinant
 CC protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial
 CC vaccine. The recombinant protein comprises, melittin signal peptide,
 CC (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes
 CC from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-
 CC 2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1),
 CC MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175
 CC (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific
 CC antigen, Pfg27. These epitopes were obtained at different stages of the
 CC life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic
 CC activity and can used for treatment and prevention of malarial
 CC infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P.
 CC falciparum in biological samples
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

RESULT 12
 AAY84427

ID AAY84427 standard; peptide; 15 AA.
 XX
 AC AAY84427;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of the tetanus toxoid P2 epitope.
 XX
 KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;
 KW osteoporosis; bone resorption; tetanus toxoid P2 epitope.
 XX
 OS Clostridium tetani.
 XX
 PN WO200015807-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 13-SEP-1999; 99WO-DK000481.
 XX
 PR 15-SEP-1998; 98DK-00001164.
 PR 02-OCT-1998; 98US-0102896P.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Halkier T, Haaning J;
 XX
 DR WPI; 2000-271444/23.
 XX
 PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to
 PT treat, prevent and ameliorate osteoporosis.
 XX
 PS Example; Page 106; 110pp; English.
 XX
 CC The present sequence represents the tetanus toxoid P2 epitope. It is used
 CC to create a fusion protein with murine osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of OPGL
 CC activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 13

AAAY82637

ID AAY82637 standard; peptide; 15 AA.

XX

AC AAY82637;

XX

DT 07-AUG-2000 (first entry)

XX

DE Tetanus toxoid T cell epitope peptide SEQ ID NO:13.

XX

KW T cell epitope; B cell epitope; allergy; allergen; antigenic;

KW antiallergic; antiasthmatic; antiinflammatory; dermatological;

KW immunosuppressive; vaccine; rhinitis; sinusitis; bronchial asthma;

KW atopic dermatitis; acute urticaria; chronic urticaria;

KW gastro-intestinal syndrome; food allergen; oro-pharyngeal syndrome;

KW anaphylactic reaction; drug hypersensitivity; allergic reaction.

XX

OS Clostridium tetani.

OS Synthetic.

XX

PN WO200006694-A2.

XX

PD 10-FEB-2000.

XX

PF 20-JUL-1999; 99WO-BE000092.

XX

PR 30-JUL-1998; 98EP-00870167.

XX

PA (UNIO) UCB SA.

XX

PI Saint-Remy J, Jacquemin M;

XX

DR WPI; 2000-422470/36.

XX

PT New compound for prevention and treatment of allergies comprises at least
PT one allergen antigenic determinant recognized by a B cell and at least
PT one antigenic determinant which does not trigger T cell activation.

XX

PS Example 6; Page 30; 50pp; English.

XX

CC The present invention describes a compound (I) for the prevention and/or
CC treatment of allergy. The compound comprises at least one allergen
CC antigenic determinant (i) recognised by a B cell or an antibody secreted
CC by a B cell of a non-atopic individual and at least one antigenic
CC determinant (ii) different from the allergen that triggers T cell
CC activation. (I) has antiallergic, antiasthmatic. antiinflammatory.
CC dermatological and immunosuppressive activities, and can be used in a
CC vaccine. (I) may be used in a pharmaceutical or cosmetic medicament to
CC treat and/or prevent allergies or a disease of allergic origin,
CC especially hypersensitivities. These include rhinitis, sinusitis,
CC bronchial asthma, atopic dermatitis, some forms of acute and chronic
CC urticaria, gastro-intestinal syndromes associated with the ingestion of

CC food allergens, oro-pharyngeal syndrome, anaphylactic reactions
CC associated with drug hypersensitivities and/or a mixture of these. The
CC use of (I) in the treatment of allergic conditions avoids the need for
CC drug treatment, which often causes undesirable side-effects. Also, prior
CC art drug therapies alleviate symptoms, but do not influence their causes,
CC however (I) actually combats the cause of an allergic reaction. The
CC present sequence represents a peptide, which is used in an example from
CC the present invention

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 14

AAY44763

ID AAY44763 standard; peptide; 15 AA.

XX

AC AAY44763;

XX

DT 04-MAY-2000 (first entry)

XX

DE Tetanus toxoid protein derived T-cell activating epitope P2.

XX

KW Surface layer protein; S-layer secretion signal; antibiotic; vaccine;
KW recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff;
KW antibacterial enzyme; surface glycoprotein; T-cell activating epitope;
KW P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.

XX

OS Clostridium tetani.

XX

PN WO200004170-A1.

XX

PD 27-JAN-2000.

XX

PF 14-JUL-1999; 99WO-CA000637.

XX

PR 14-JUL-1998; 98CA-02237704.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX

PI Smit J;

XX

DR WPI; 2000-182434/16.

XX

PT Cleavage of Caulobacter produced recombinant fusion proteins useful for
PT producing vaccine peptides.

XX

PS Example 2; Page 16; 33pp; English.

XX

CC The patent discloses a method for cleaving a recombinant fusion protein

CC which is produced by Caulobacter and consists of Caulobacter surface
CC layer (S-layer) protein (containing the C-terminal secretion signal) and
CC a target protein heterologous to Caulobacter. The cleavage of target
CC protein from the S-layer protein is carried out under mild acid
CC conditions so that cleavage occurs at aspartate-proline dipeptide site
CC without solubilising the protein. The cleavage is accomplished while the
CC fusion protein is in an insoluble aggregate form which facilitates
CC purification of the protein. The method is useful for producing pure
CC proteins including recombinant human and animal therapeutic antibiotic
CC and vaccine peptides, enzymes, protein polymers, and antibacterial
CC enzymes for foodstuffs. The present sequence is a T-cell activating
CC epitope P2 derived from tetanus toxoid protein. This sequence was fused
CC to a DNA encoding a fragment of Infectious pancreatic necrosis virus
CC surface glycoprotein which is a vaccine candidate. This chimeric protein
CC was in turn fused to DNA encoding C. crescentus S-layer secretion signal
CC (corresponds to the C-terminal portion of the S-layer protein from amino
CC acid 690 onwards and contains native Asp-Pro site) for construction of a
CC recombinant fusion construct which is expressed in Caulobacter and then
CC cleaved to recover the vaccine candidate protein

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 15

AAB45511

ID AAB45511 standard; protein; 15 AA.

XX

AC AAB45511;

XX

DT 26-FEB-2001 (first entry)

XX

DE Tetanus P2 epitope SEQ ID NO: 23.

XX

KW Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;

KW cancer; eosinophilia; vaccine; allergic rhinitis.

XX

OS Clostridium tetani.

XX

PN WO200065058-A1.

XX

PD 02-NOV-2000.

XX

PF 19-APR-2000; 2000WO-DK000205.

XX

PR 23-APR-1999; 99DK-00000552.

PR 06-MAY-1999; 99US-0132811P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Klysner S;
 XX
 DR WPI; 2000-672791/65.
 XX
 PT Down-regulating interleukin 5 (IL-5) activity in humans by administering
 PT IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or
 PT amelioration of asthma or other chronic allergic conditions.
 XX
 PS Example 1; Page 137; 172pp; English.
 XX
 CC The present invention is concerned with methods of treating asthma,
 CC eosinophilia, allergic rhinitis and other allergic diseases. These
 CC involve the use of interleukin-5 (IL-5) analogues and modified IL-5
 CC proteins and their coding sequences to down-regulate IL-5 activity and
 CC thus reduce eosinophil numbers. The allergic diseases may be treated
 CC using autovaccines, nucleic acid vaccines or live vaccines. In addition,
 CC it is possible that they may be used in the treatment of cancer and
 CC helminthic infections
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

Search completed: August 13, 2004, 09:12:40
 Job time : 6.38828 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:09:23 ; Search time 1.02564 Seconds
 (without alignments)
 755.030 Million cell updates/sec

Title: US-09-785-215-4
 Perfect score: 74
 Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	74	100.0	15	2	US-08-319-704-10	Sequence 10, Appl
2	74	100.0	15	2	US-08-661-052-6	Sequence 6, Appli
3	74	100.0	15	2	US-08-460-502-7	Sequence 7, Appli
4	74	100.0	15	3	US-09-046-373-2	Sequence 2, Appli
5	74	100.0	15	3	US-09-188-082-6	Sequence 6, Appli
6	74	100.0	15	4	US-09-364-088-6	Sequence 6, Appli
7	74	100.0	15	4	US-09-102-716-6	Sequence 6, Appli
8	74	100.0	15	4	US-09-148-711A-7	Sequence 7, Appli
9	74	100.0	15	4	US-08-716-249-4	Sequence 4, Appli
10	74	100.0	15	4	US-09-362-731A-13	Sequence 13, Appl
11	74	100.0	15	4	US-09-396-937-34	Sequence 34, Appl

12	74	100.0	15	4	US-09-405-986A-1	Sequence 1, Appli
13	74	100.0	15	5	PCT-US93-11703-69	Sequence 69, Appl
14	74	100.0	16	3	US-09-248-588-55	Sequence 55, Appl
15	74	100.0	17	1	US-08-446-692-4	Sequence 4, Appli
16	74	100.0	17	2	US-08-488-351A-4	Sequence 4, Appli
17	74	100.0	17	3	US-09-100-409A-40	Sequence 40, Appl
18	74	100.0	17	4	US-08-472-701-23	Sequence 23, Appl
19	74	100.0	17	5	PCT-US95-08596-23	Sequence 23, Appl
20	74	100.0	17	5	PCT-US95-13841-7	Sequence 7, Appli
21	74	100.0	27	1	US-08-446-692-13	Sequence 13, Appl
22	74	100.0	27	2	US-08-488-351A-13	Sequence 13, Appl
23	74	100.0	31	4	US-09-362-731A-1	Sequence 1, Appli
24	74	100.0	31	5	PCT-US93-11703-63	Sequence 63, Appl
25	74	100.0	32	4	US-09-362-731A-5	Sequence 5, Appli
26	74	100.0	37	1	US-08-446-692-57	Sequence 57, Appl
27	74	100.0	37	1	US-08-446-692-63	Sequence 63, Appl
28	74	100.0	37	2	US-08-488-351A-57	Sequence 57, Appl
29	74	100.0	37	2	US-08-488-351A-63	Sequence 63, Appl
30	74	100.0	47	1	US-08-446-692-35	Sequence 35, Appl
31	74	100.0	47	2	US-08-488-351A-35	Sequence 35, Appl
32	74	100.0	50	4	US-08-945-289-8	Sequence 8, Appli
33	74	100.0	137	4	US-09-362-731A-3	Sequence 3, Appli
34	74	100.0	173	4	US-09-396-937-18	Sequence 18, Appl
35	74	100.0	182	4	US-09-396-937-16	Sequence 16, Appl
36	74	100.0	853	4	US-08-913-880C-17	Sequence 17, Appl
37	74	100.0	858	4	US-08-913-880C-16	Sequence 16, Appl
38	74	100.0	860	4	US-08-913-880C-15	Sequence 15, Appl
39	74	100.0	862	4	US-08-913-880C-14	Sequence 14, Appl
40	74	100.0	865	4	US-08-913-880C-13	Sequence 13, Appl
41	74	100.0	866	4	US-08-913-880C-12	Sequence 12, Appl
42	74	100.0	874	4	US-08-913-880C-11	Sequence 11, Appl
43	74	100.0	875	4	US-08-913-880C-10	Sequence 10, Appl
44	74	100.0	1315	4	US-08-913-880C-1	Sequence 1, Appli
45	70	94.6	14	1	US-08-186-266-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-319-704-10

; Sequence 10, Application US/08319704

; Patent No. 5814617

; GENERAL INFORMATION:

; APPLICANT: Hoffman, Stephen L.

; APPLICANT: Charoenvit, Yupin

; APPLICANT: Hedstrom, Richard C.

; APPLICANT: Doolan, Denise L.

; TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and

; TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Naval Medical R & D Command

; STREET: Bldg 1, T-12, 8901 Wisconsin Avenue

; CITY: Bethesda

; STATE: Maryland

; COUNTRY: U.S.A

```

; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,704
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: A. David Spevack
; REGISTRATION NUMBER: 24,743
; REFERENCE/DOCKET NUMBER: 75,206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-6759
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-319-704-10

```

```

Query Match      100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15

```

RESULT 2

```

US-08-661-052-6
; Sequence 6, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-661-052-6

```

```

Query Match          100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15

```

RESULT 3

US-08-460-502-7

```

; Sequence 7, Application US/08460502
; Patent No. 5843464
; GENERAL INFORMATION:
; APPLICANT: Bakaletz, Lauren O.
; APPLICANT: Kaumaya, Parvin T.
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter and Griswold
; STREET: 800 Superior Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2688
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,502
; FILING DATE:
; CLASSIFICATION: 424

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Golrick, Mary E.
; REGISTRATION NUMBER: 34,829
; REFERENCE/DOCKET NUMBER: 22727/00120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 622-8458
; TELEFAX: (216) 241-0816
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-502-7

```

```

Query Match          100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15

```

RESULT 4

US-09-046-373-2

```

; Sequence 2, Application US/09046373
; Patent No. 6235714
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Larry J. Smith
; APPLICANT: Gennady Gololobov
; TITLE OF INVENTION: Methods for Identifying Inducers and
; TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and
Their
; TITLE OF INVENTION: Use
; FILE REFERENCE: UNMC 63123
; CURRENT APPLICATION NUMBER: US/09/046,373
; CURRENT FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-046-373-2

```

```

Query Match          100.0%; Score 74; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15

```


RESULT 5

US-09-188-082-6

; Sequence 6, Application US/09188082
 ; Patent No. 6270765
 ; GENERAL INFORMATION:
 ; APPLICANT: Yashwant M. Deo
 ; APPLICANT: Joel Goldstein
 ; APPLICANT: Robert Graziano
 ; APPLICANT: Chezian Somasundaram
 ; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
 ; TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/188,082
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/661,052
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Arnold, Beth E.
 ; REGISTRATION NUMBER: 35,430
 ; REFERENCE/DOCKET NUMBER: MXI-043CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal

US-09-188-082-6

Query Match 100.0%; Score 74; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

RESULT 6

US-09-364-088-6

```

; Sequence 6, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
;   APPLICANT: Yashwant M. Deo, et al.
;   TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
;   TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD, LLP
;     STREET: 28 State Street, 24th Floor
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/364,088
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 09/188,082
;     FILING DATE: 07-JUNE-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/484,172
;     FILING DATE: 07-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Remillard, Jane E.
;     REGISTRATION NUMBER: 38,872
;     REFERENCE/DOCKET NUMBER: MXI-043CP2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617)227-7400
;     TELEFAX: (617)742-7414
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     FRAGMENT TYPE: internal
US-09-364-088-6

```

```

Query Match          100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||||||||||
Db      1 QYIKANSKFIGITEL 15

```

```

RESULT 7
US-09-102-716-6
; Sequence 6, Application US/09102716
; Patent No. 6395272

```

```

; GENERAL INFORMATION:
;   APPLICANT: Yashwant M. Deo
;               Joel Goldstein
;               Robert Graziano
;               Chezian Somasundaram
;   TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
;                       OF ANTI-Fc RECEPTOR ANTIBODIES
;   NUMBER OF SEQUENCES: 16
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: LAHIVE & COCKFIELD
;       STREET: 60 State Street, Suite 510
;       CITY: Boston
;       STATE: Massachusetts
;       COUNTRY: USA
;       ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/102,716
;       FILING DATE: 22-Jun-1998
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/661,052
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Arnold, Beth E.
;       REGISTRATION NUMBER: 35,430
;       REFERENCE/DOCKET NUMBER: MXI-043CP
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (617)227-7400
;       TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 15 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       FRAGMENT TYPE: internal
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-102-716-6

```

```

Query Match      100.0%;  Score 74;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 2.3e-07;
Matches   15;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15

```

```

RESULT 8
US-09-148-711A-7
; Sequence 7, Application US/09148711A
; Patent No. 6436405
; GENERAL INFORMATION:

```

```
; APPLICANT: The Ohio State University
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
; FILE REFERENCE: 18525-04010
; CURRENT APPLICATION NUMBER: US/09/148,711A
; CURRENT FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 08/460,502
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: clostridium tetani
US-09-148-711A-7
```

```
Query Match          100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15
```

RESULT 9

US-08-716-249-4

```
; Sequence 4, Application US/08716249
; Patent No. 6455244
; GENERAL INFORMATION:
; APPLICANT: Guichard, Gilles
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Regenmortel, Marc
; TITLE OF INVENTION: Retropeptides, Antibodies Thereto, and
; TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spencer & Frank
; STREET: 1100 New York Avenue, Suite 300E
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,249
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00292
; FILING DATE: 13-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Calvetti, Frederick F.
; REGISTRATION NUMBER: 28,557
```

```
; REFERENCE/DOCKET NUMBER: GROFO 7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)414-4000
; TELEFAX: (202)414-4040
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-716-249-4
```

```
Query Match          100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 QYIKANSKFIGITEL 15
        |||||||||||||
Db      1 QYIKANSKFIGITEL 15
```

RESULT 10

US-09-362-731A-13

```
; Sequence 13, Application US/09362731A
; Patent No. 6602509
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE
TREATMENT OF ALLERGY
; FILE REFERENCE: 99-0720*/LC/01699
; CURRENT APPLICATION NUMBER: US/09/362,731A
; CURRENT FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-09-362-731A-13
```

```
Query Match          100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 QYIKANSKFIGITEL 15
        |||||||||||||
Db      1 QYIKANSKFIGITEL 15
```

RESULT 11

US-09-396-937-34

```
; Sequence 34, Application US/09396937
```

; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-396-937-34

Query Match 100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 12

US-09-405-986A-1
; Sequence 1, Application US/09405986A
; Patent No. 6676946
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/09/405,986A
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-405-986A-1

Query Match 100.0%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 13

PCT-US93-11703-69

; Sequence 69, Application PC/TUS9311703
; GENERAL INFORMATION:
; APPLICANT: Chiron Mimotopes Pty. Ltd.
; TITLE OF INVENTION: T-Cell Epitopes
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Grant D. Green
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11703
; FILING DATE: 28-DEC-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,852
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 0222.101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2706
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-11703-69

Query Match 100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 14

US-09-248-588-55

; Sequence 55, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Clostridium tetani
; PUBLICATION INFORMATION:
; JOURNAL: Vaccine
; VOLUME: 15
; ISSUE: 4
; PAGES: 377-
; DATE: 1997
US-09-248-588-55

Query Match 100.0%; Score 74; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 15

US-08-446-692-4

; Sequence 4, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for
vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-4

Query Match 100.0%; Score 74; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 3 QYIKANSKFIGITEL 17

Search completed: August 13, 2004, 09:17:35
Job time : 1.02564 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:08:23 ; Search time 0.824176 Seconds
 (without alignments)
 1750.686 Million cell updates/sec

Title: US-09-785-215-4
 Perfect score: 74
 Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	74	100.0	1315	1	BTCLTN	tentoxilysin (EC 3
2	44.5	60.1	244	2	S29982	class II histocomp
3	44	59.5	66	2	S31029	gene 84 protein -
4	43	58.1	180	2	G86826	diamine N-acetyltr
5	43	58.1	899	2	T42976	hypothetical prote
6	42.5	57.4	1060	2	S06286	major merozoite su
7	42.5	57.4	1086	2	S16752	major merozoite su
8	42.5	57.4	1701	2	A54498	major merozoite su
9	42.5	57.4	1701	2	A26868	major merozoite su
10	42.5	57.4	1726	1	SAZQGM	major merozoite su
11	42.5	57.4	1726	2	A45948	major merozoite su
12	42	56.8	1333	2	S38635	blastopia polyprot
13	41	55.4	123	2	G48677	Ig heavy chain V-D

14	41	55.4	447	2	H97146	siderophore/Surfac
15	41	55.4	899	2	G36812	hypothetical prote
16	40.5	54.7	245	2	S29980	class II histocomp
17	40	54.1	79	2	D85794	hypothetical prote
18	40	54.1	194	2	G64026	[acyl-carrier-prot
19	40	54.1	601	1	A55485	oligopeptidase (EC
20	40	54.1	601	2	G86840	oligoendopeptidase
21	40	54.1	644	2	S46746	hypothetical prote
22	39	52.7	102	2	PH1491	Ig heavy chain V r
23	39	52.7	119	2	PH1516	Ig heavy chain V r
24	39	52.7	119	2	PH1518	Ig heavy chain V r
25	39	52.7	119	2	PH1519	Ig heavy chain V r
26	39	52.7	123	2	F48677	Ig heavy chain V-D
27	39	52.7	135	2	PH1494	Ig heavy chain V r
28	39	52.7	140	2	PH1488	Ig heavy chain V r
29	39	52.7	189	2	G97978	conserved hypothet
30	39	52.7	213	1	KIYMC	adenylate kinase (
31	39	52.7	326	2	B71808	type II restrictio
32	39	52.7	349	2	T43043	probable acetyl-Co
33	39	52.7	423	2	F64690	type IIS restricti
34	39	52.7	505	2	C90569	hypothetical prote
35	38	51.4	188	2	H71875	hypothetical prote
36	38	51.4	188	2	A64639	hypothetical prote
37	38	51.4	256	2	F64472	hypothetical prote
38	38	51.4	287	2	F70361	tRNA-pseudouridine
39	38	51.4	381	2	F71196	probable hexosyltr
40	38	51.4	383	2	T51466	hypothetical prote
41	38	51.4	424	2	T29127	hypothetical prote
42	38	51.4	501	2	A86158	endo-1,4-beta gluc
43	38	51.4	501	2	T52135	cellulase (EC 3.2.
44	38	51.4	561	2	E82395	methyl-accepting c
45	38	51.4	572	1	HNNZ80	hemagglutinin-neur

ALIGNMENTS

RESULT 1

BTCLTN

tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani

N;Alternate names: tetanus neurotoxin

C;Species: Clostridium tetani

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 03-Jun-2002

C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364

R;Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M.; Habermann, E.; Niemann, H.

EMBO J. 5, 2495-2502, 1986

A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botulinum toxins.

A;Reference number: A25689; MUID:87053814; PMID:3536478

A;Accession: A25689

A;Molecule type: DNA

A;Residues: 1-1315 <EIS>

A;Cross-references: GB:X04436; NID:g40769; PIDN:CAA28033.1; PID:g40770

R;Fairweather, N.F.; Lyness, V.A.

Nucleic Acids Res. 14, 7809-7812, 1986

A;Title: The complete nucleotide sequence of tetanus toxin.

A;Reference number: A25757; MUID:87040747; PMID:3774547
 A;Accession: A25757
 A;Molecule type: DNA
 A;Residues: 1-1315 <FAI>
 A;Cross-references: GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g40774
 A;Experimental source: strain CN3911
 R;Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
 J. Bacteriol. 165, 21-27, 1986
 A;Title: Cloning, nucleotide sequencing, and expression of tetanus toxin
 fragment C in Escherichia coli.
 A;Reference number: A25194; MUID:86085672; PMID:3510187
 A;Accession: A25194
 A;Molecule type: DNA
 A;Residues: 743-1315 <FA2>
 A;Cross-references: GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:g144921
 A;Accession: B25194
 A;Molecule type: protein
 A;Residues: 865-894 <FA3>
 R;Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
 Infect. Immun. 57, 3588-3593, 1989
 A;Title: Isolation, purification, and characterization of fragment B, the NH-2-
 terminal half of the heavy chain of tetanus toxin.
 A;Reference number: A60759; MUID:90035436; PMID:2478476
 A;Accession: A60759
 A;Molecule type: protein
 A;Residues: 461-475 <MAT>
 R;Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin,
 G.
 J. Immunol. 142, 394-402, 1989
 A;Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
 A;Reference number: JS0098; MUID:89093918; PMID:2463305
 A;Contents: annotation; epitope region
 R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.;
 DasGupta, B.R.; Montecucco, C.
 Nature 359, 832-835, 1992
 A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by
 proteolytic cleavage of synaptobrevin.
 A;Reference number: S27125; MUID:93063293; PMID:1331807
 A;Contents: annotation
 R;de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
 Eur. J. Biochem. 229, 61-69, 1995
 A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus
 neurotoxin.
 A;Reference number: S69348; MUID:95262688; PMID:7744050
 A;Accession: S69348
 A;Molecule type: protein
 A;Residues: 2-31 <DEF>
 C;Comment: The source of this protein was an extrachromosomal plasmid.
 C;Comment: The precursor is cleaved by endogenous proteinase activity to form
 light (fragment A) and heavy (fragment B.C) chains that are covalently linked by
 an interchain disulfide bond (the individual chains are not toxic when
 separated). The amino end of the heavy chain (fragment B) can be separated from
 the carboxyl end (fragment C) by papain.
 C;Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to
 gangliosides and may target the toxin to the motor end plate. Fragment A is a
 zinc-dependent endopeptidase.

C;Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized, and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of synaptobrevin (vesicle-associated membrane protein 2).

C;Function:

A;Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2

C;Superfamily: tetanus toxin

C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc

F;2-457/Product: tentoxylisin light chain (fragment A) #status predicted <TTL>

F;461-1315/Product: tentoxylisin heavy chain (fragment B.C) #status experimental <TTH>

F;461-864/Domain: channel forming (fragment B) #status predicted <TXB>

F;865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>

F;233,237/Binding site: zinc (His) #status predicted

F;234/Active site: Glu #status predicted

Query Match 100.0%; Score 74; DB 1; Length 1315;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 830 QYIKANSKFIGITEL 844

RESULT 2

S29982

class II histocompatibility antigen - Atlantic salmon

C;Species: Salmo salar (Atlantic salmon)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999

C;Accession: S29982

R;Hordvik, I.

submitted to the EMBL Data Library, October 1992

A;Reference number: S29980

A;Accession: S29982

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-244 <HOR>

A;Cross-references: EMBL:X70166; NID:g64369; PID:g64370

C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 60.1%; Score 44.5; DB 2; Length 244;
Best Local Similarity 55.6%; Pred. No. 1.8;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
:| |: | | | | | | | |
Db 51 EYIRENSTVGKFVGYTEL 68

RESULT 3

S31029

gene 84 protein - Mycobacterium phage L5

C;Species: Mycobacterium phage L5

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
 C;Accession: S31029
 R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
 Mol. Microbiol. 7, 407-417, 1993
 A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic transformation of mycobacteria.
 A;Reference number: S30949; MUID:93211283; PMID:8459767
 A;Accession: S31029
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-66 <DON>
 A;Cross-references: EMBL:Z18946; NID:g15859; PIDN:CAA79460.1; PID:e59702; PID:g579152
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
 C;Genetics:
 A;Gene: 84
 A;Start codon: GTG

Query Match 59.5%; Score 44; DB 2; Length 66;
 Best Local Similarity 57.1%; Pred. No. 0.58;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 YIKANSKFIGITEL 15
 ||| | ||:| |:
 Db 50 YIKRNGKFVGTWEV.63

RESULT 4

G86826

diamine N-acetyltransferase (EC 2.3.1.57) [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)

N;Alternate names: spermidine acetyltransferase

C;Species: *Lactococcus lactis* subsp. *lactis*

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 17-May-2002

C;Accession: G86826

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.D.; Sorokin, A.

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. *lactis* IL1403.

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: G86826

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-180 <STO>

A;Cross-references: GB:AE005176; PID:g12724622; PIDN:AAK05713.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: yqfF

C;Superfamily: *Escherichia coli* ribosomal-protein-alanine N-acetyltransferase rimJ

C;Keywords: acyltransferase; coenzyme A

Query Match 58.1%; Score 43; DB 2; Length 180;
 Best Local Similarity 69.2%; Pred. No. 2.5;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 IKANSKFIGITEL 15
 |:|| ||||, ||
Db 65 IEANDTFIGIVEL 77

RESULT 5

T42976

hypothetical protein 63 - ateline herpesvirus 3 (strain 73)

C;Species: ateline herpesvirus 3

A;Variety: strain 73

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C;Accession: T42976

R;Albrecht, J.C.; Fleckenstein, B.

submitted to the EMBL Data Library, August 1998

A;Description: Primary structure of the herpesvirus ateles genome.

A;Reference number: Z22274

A;Accession: T42976

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-899 <ALB>

A;Cross-references: EMBL:AF083424; PIDN:AAC95587.1

A;Experimental source: strain 73

Query Match 58.1%; Score 43; DB 2; Length 899;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITE 14
 ||| :|| | | ||
Db 124 QYITSNSTFTGQTE 137

RESULT 6

S06286

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain RO-33 Ghana) (fragment)

N;Alternate names: 190K protein; polymorphic schizont antigen

C;Species: Plasmodium falciparum

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jun-2000

C;Accession: S06286

R;Certa, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.

EMBO J. 6, 4137-4142, 1987

A;Title: A naturally occurring gene encoding the major surface antigen precursor p190 of Plasmodium falciparum lacks tripeptide repeats.

A;Reference number: S06286; MUID:88166657; PMID:3327688

A;Accession: S06286

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-1060 <CER>

C;Superfamily: major merozoite surface antigen

C;Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1060;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:| | | | | |:
Db 983 QFVKSNSKVITGLTE 997

RESULT 7

S16752

major merozoite surface antigen MSA-1 - malaria parasite (Plasmodium falciparum) (fragments)

N;Alternate names: polymorphic schizont antigen p190

C;Species: Plasmodium falciparum

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000

C;Accession: A44865; S16752

R;Olafsson, P.; Matile, H.; Certa, U.

Exp. Parasitol. 74, 381-389, 1992

A;Title: Plasmodium falciparum: the repetitive MSA-1 surface protein of the RO-71 isolate is recognized by mouse antibody against the nonrepetitive repeat block of RO-33.

A;Reference number: A44865; MUID:92275047; PMID:1592091

A;Accession: A44865

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1086 <OLA>

A;Cross-references: EMBL:X61930

A;Experimental source: isolate RO-71

C;Genetics:

A;Gene: MSA1

C;Superfamily: major merozoite surface antigen

C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Query Match 57.4%; Score 42.5; DB 2; Length 1086;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:| | | | | |:
Db 1009 QFVKSNSKVITGLTE 1023

RESULT 8

A54498

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (isolate FC27)

C;Species: Plasmodium falciparum

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000

C;Accession: A54498

R;Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.;

Brown, G.V.; Anders, R.F.; Kemp, D.J.

Mol. Biochem. Parasitol. 27, 291-302, 1988

A;Title: Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.

A;Reference number: A54498; MUID:88142999; PMID:2449612

A;Accession: A54498

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1701 <PET>

A;Cross-references: GB:M19143; NID:g160412; PIDN:AAA29653.1; PID:g160413

C;Superfamily: major merozoite surface antigen

C;Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1701;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:|||| | |::||
Db 1001 QFVKSNSKVITGLTE 1015

RESULT 9

A26868

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain MAD20/papua New Guinea)

C;Species: Plasmodium falciparum

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000

C;Accession: A26868

R;Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.

J. Mol. Biol. 195, 273-287, 1987

A;Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium falciparum.

A;Reference number: A26868; MUID:88011243; PMID:3079521

A;Accession: A26868

A;Molecule type: DNA

A;Residues: 1-1701 <TAN>

C;Superfamily: major merozoite surface antigen

C;Keywords: surface antigen

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-1701/Product: major merozoite surface antigen #status predicted <MAT>

Query Match 57.4%; Score 42.5; DB 2; Length 1701;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:|||| | |::||
Db 1001 QFVKSNSKVITGLTE 1015

RESULT 10

SAZQGM

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain CAMP/Malaysia)

N;Alternate names: 195K glycoprotein

C;Species: Plasmodium falciparum

C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000

C;Accession: A23386; S06361

R;Weber, J.L.; Leininger, W.M.; Lyon, J.A.

Nucleic Acids Res. 14, 3311-3323, 1986

A;Title: Variation in the gene encoding a major merozoite surface antigen of the human malaria parasite Plasmodium falciparum.

A;Reference number: A23386; MUID:86205236; PMID:3517809

A;Accession: A23386

A;Molecule type: DNA

A;Residues: 1-1104 <WEB1>

A;Cross-references: EMBL:X03831
R;Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
A;Title: Merozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.
A;Reference number: S06361; MUID:88143999; PMID:3278296
A;Accession: S06361
A;Molecule type: DNA
A;Residues: 1104-1726 <WEB2>
A;Cross-references: EMBL:X03831
C;Comment: The merozoite stages of different strains have strain-specific surface antigens that are involved in strain-specific immunity.
C;Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The merozoite stage can be recovered from the blood.
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F;67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-T)
F;757-765/Region: 3-residue repeats (T-E-E)
F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.4%; Score 42.5; DB 1; Length 1726;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:| | | | | | | |
Db 1026 QFVKSNSKVITGLTE 1040

RESULT 11

A45948
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain Uganda-Palo Alto)
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C;Accession: A45948
R;Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A;Title: Plasmodium falciparum: gene structure and hydropathy profile of the major merozoite surface antigen (gp195) of the Uganda-Palo Alto isolate.
A;Reference number: A45948; MUID:89005525; PMID:3049134
A;Accession: A45948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1726 <CHA>
A;Cross-references: GB:M37213
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1726;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14

Db |::|:| | | | |
1026 QFVKSNSKVVITGLTE 1040

RESULT 12

S38635

blastopia polyprotein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

C;Accession: S38635

R;Frommer, G.; Schuh, R.; Jdckle, H.

submitted to the EMBL Data Library, November 1993

A;Description: Localized expression of a novel micropia-like element in the blastoderm of Drosophila melanogaster is dependent on the anterior morphogen bicoid.

A;Reference number: S38635

A;Accession: S38635

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1333 <FRO>

A;Cross-references: EMBL:Z27119; NID:g415797; PID:g415798

C;Genetics:

A;Gene: FlyBase:micropia

A;Cross-references: FlyBase:FBgn0014947

C;Keywords: polyprotein

Query Match 56.8%; Score 42; DB 2; Length 1333;
Best Local Similarity 53.3%; Pred. No. 29;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 :|::| || || ||
Db 127 KYVQARSKMIGSAEL 141

RESULT 13

G48677

Ig heavy chain V-D-J region (419.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: G48677

R;Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.;

Hasemann, C.A.; Capra, J.D.; Meek, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993

A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies derived from idiotype-negative mice bearing a light chain polymorphism.

A;Reference number: A48677; MUID:94022404; PMID:8415731

A;Accession: G48677

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-123 <TAS>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 55.4%; Score 41; DB 2; Length 123;

Best Local Similarity 64.3%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 YIKANSKFIGITEL 15
||| | || | | |
Db 57 YIKYNEKFKGTTTL 70

RESULT 14

H97146

siderophore/Surfactin synthetase related protein [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: H97146

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: H97146

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-447 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79963.1; PID:g15024986; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC2004

Query Match 55.4%; Score 41; DB 2; Length 447;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIG 11
:||: | |||
Db 291 KYIRTNKKFIG 301

RESULT 15

G36812

hypothetical protein ORF63 - saimiriine herpesvirus 1 (strain 11)

C;Species: saimiriine herpesvirus 1

A;Note: host Saimiri sciureus (common squirrel monkey)

C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999

C;Accession: G36812

R;Albrecht, J.

submitted to the EMBL Data Library, January 1992

A;Description: Primary structure of the herpesvirus saimiri genome.

A;Reference number: A36806

A;Accession: G36812

A;Molecule type: DNA

A;Residues: 1-899 <ALB>

A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45686.1; PID:g60384

R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wittmann, S.; Craxton, M.A.; Coleman, H.; Fleckenstein, B.; Honess, R.W.

J. Virol. 66, 5047-5058, 1992

A;Title: Primary structure of the herpesvirus saimiri genome.

A;Reference number: A37309; MUID:92333688; PMID:1321287

A;Contents: annotation; protein-coding frames

A;Note: neither protein nor nucleotide sequence is given

C;Genetics:

A;Gene: 63

Query Match 55.4%; Score 41; DB 2; Length 899;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITE 14

||| :|: | |::|

Db 124 QYITSNATFTGLSE 137

Search completed: August 13, 2004, 09:16:31

Job time : 2.82418 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:15:49 ; Search time 2.82051 Seconds
(without alignments)
1669.522 Million cell updates/sec

Title: US-09-785-215-4
Perfect score: 74
Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	74	100.0	15	9	US-09-862-849-2	Sequence 2, Appli
2	74	100.0	15	9	US-09-785-215-4	Sequence 4, Appli
3	74	100.0	15	10	US-09-405-986-1	Sequence 1, Appli
4	74	100.0	15	12	US-10-668-400-1	Sequence 1, Appli
5	74	100.0	15	12	US-10-114-716A-2	Sequence 2, Appli
6	74	100.0	15	14	US-10-204-362-4	Sequence 4, Appli
7	74	100.0	15	14	US-10-223-711-7	Sequence 7, Appli
8	74	100.0	15	14	US-10-237-656-13	Sequence 13, Appl
9	74	100.0	15	14	US-10-223-809A-4	Sequence 4, Appli
10	74	100.0	15	14	US-10-261-446-19	Sequence 19, Appl
11	74	100.0	15	14	US-10-239-313A-618	Sequence 618, App
12	74	100.0	15	14	US-10-295-074-3	Sequence 3, Appli
13	74	100.0	15	15	US-10-372-111-7	Sequence 7, Appli
14	74	100.0	15	16	US-10-261-445B-19	Sequence 19, Appl
15	74	100.0	15	16	US-10-664-801-34	Sequence 34, Appl
16	74	100.0	15	16	US-10-699-517-9	Sequence 9, Appli
17	74	100.0	15	16	US-10-441-779C-11	Sequence 11, Appl
18	74	100.0	16	9	US-09-848-834A-2	Sequence 2, Appli
19	74	100.0	16	10	US-09-930-915A-64	Sequence 64, Appl
20	74	100.0	16	14	US-10-082-014-145	Sequence 145, App
21	74	100.0	16	14	US-10-372-076-175	Sequence 175, App
22	74	100.0	16	16	US-10-699-517-16	Sequence 16, Appl
23	74	100.0	16	16	US-10-699-517-18	Sequence 18, Appl
24	74	100.0	16	16	US-10-699-517-31	Sequence 31, Appl
25	74	100.0	16	16	US-10-806-006-64	Sequence 64, Appl
26	74	100.0	17	10	US-09-865-294-3	Sequence 3, Appli
27	74	100.0	17	12	US-10-457-082-14	Sequence 14, Appl
28	74	100.0	17	14	US-10-239-313A-619	Sequence 619, App
29	74	100.0	17	15	US-10-346-563-23	Sequence 23, Appl
30	74	100.0	17	15	US-10-411-544-5	Sequence 5, Appli
31	74	100.0	17	15	US-10-321-717-23	Sequence 23, Appl
32	74	100.0	19	14	US-10-239-313A-620	Sequence 620, App
33	74	100.0	22	16	US-10-699-517-34	Sequence 34, Appl
34	74	100.0	22	16	US-10-699-517-37	Sequence 37, Appl
35	74	100.0	22	16	US-10-699-517-53	Sequence 53, Appl
36	74	100.0	25	16	US-10-441-779C-14	Sequence 14, Appl
37	74	100.0	25	16	US-10-441-779C-15	Sequence 15, Appl
38	74	100.0	25	16	US-10-441-779C-16	Sequence 16, Appl
39	74	100.0	27	14	US-10-076-674-7	Sequence 7, Appli
40	74	100.0	27	15	US-10-355-161A-7	Sequence 7, Appli
41	74	100.0	28	9	US-09-848-834A-11	Sequence 11, Appl
42	74	100.0	31	9	US-09-848-834A-15	Sequence 15, Appl
43	74	100.0	31	14	US-10-237-656-1	Sequence 1, Appli
44	74	100.0	32	14	US-10-237-656-5	Sequence 5, Appli
45	74	100.0	37	16	US-10-699-517-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-862-849-2

; Sequence 2, Application US/09862849

; Patent No. US20020013274A1

; GENERAL INFORMATION:

; APPLICANT: Sudhir Paul

; APPLICANT: Larry J. Smith
; APPLICANT: Gennady Gololobov
; TITLE OF INVENTION: Methods for Identifying Inducers and Inhibitors of
Proteolytic
; TITLE OF INVENTION: Antibodies, Compositions and Their Uses
; FILE REFERENCE: UNMC 63123 DIV
; CURRENT APPLICATION NUMBER: US/09/862,849
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/046,373
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-862-849-2

Query Match 100.0%; Score 74; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 2

US-09-785-215-4
; Sequence 4, Application US/09785215
; Publication No. US20020187157A1
; GENERAL INFORMATION:
; APPLICANT: JENSEN, Martin Roland et al.
; TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID
; FILE REFERENCE: 3631-0107P
; CURRENT APPLICATION NUMBER: US/09/785,215
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-785-215-4

Query Match 100.0%; Score 74; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 3

US-09-405-986-1
; Sequence 1, Application US/09405986


```

; Publication No. US20030157115A1
; GENERAL INFORMATION:
; APPLICANT: BAY, Sylvie
; APPLICANT: CANTACUZENE, Daniele
; APPLICANT: LECLERC, Claude
; APPLICANT: LO-MAN, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE, VACCINE
; TITLE OF INVENTION: COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 134I US 3565
; CURRENT APPLICATION NUMBER: US/09/405,986
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 60/041,726
; EARLIER FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-405-986-1

```

```

Query Match          100.0%; Score 74; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches    15; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 QYIKANSKFIGITEL 15
        |||||
Db      1 QYIKANSKFIGITEL 15

```

RESULT 4

```

US-10-668-400-1
; Sequence 1, Application US/10668400
; Publication No. US20040058859A1
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-668-400-1

```

```

Query Match          100.0%; Score 74; DB 12; Length 15;

```

Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 5

US-10-114-716A-2

; Sequence 2, Application US/10114716A
; Publication No. US20030078203A1
; GENERAL INFORMATION:
; APPLICANT: Sudhir Paul
; APPLICANT: Yasuhiro Nishiyama
; TITLE OF INVENTION: Covalently Reactive Transition State
; TITLE OF INVENTION: Analogs and Methods of Use Thereof
; FILE REFERENCE: UTH001HB
; CURRENT APPLICATION NUMBER: US/10/114,716A
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 09/862,849
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/046,373
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/280,624
; PRIOR FILING DATE: 2001-03-31
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-114-716A-2

Query Match 100.0%; Score 74; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 6

US-10-204-362-4

; Sequence 4, Application US/10204362
; Publication No. US20030086938A1
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: No. US20030086938A1el Method For Down-Regulation Of
Amyloid
; FILE REFERENCE: 3631-0120P
; CURRENT APPLICATION NUMBER: US/10/204,362
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-204-362-4

Query Match 100.0%; Score 74; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 7

US-10-223-711-7

; Sequence 7, Application US/10223711
; Publication No. US20030113344A1
; GENERAL INFORMATION:
; APPLICANT: Bakaletz, Lauren O.
; APPLICANT: Kaumaya, Pravin T.P.
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
; FILE REFERENCE: 18525/04058
; CURRENT APPLICATION NUMBER: US/10/223,711
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/148,711
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 08/460,502
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-223-711-7

Query Match 100.0%; Score 74; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 8

US-10-237-656-13

; Sequence 13, Application US/10237656
; Publication No. US20030152581A1
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE
TREATMENT OF ALLERGY
; FILE REFERENCE: 2002-0771/LC/01699
; CURRENT APPLICATION NUMBER: US/10/237,656

; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/362,731
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-10-237-656-13

Query Match 100.0%; Score 74; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 9

US-10-223-809A-4

; Sequence 4, Application US/10223809A
; Publication No. US20030157117A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; APPLICANT: Rasmussen, Peter Birk et al.
; TITLE OF INVENTION: No. US20030157117A1 Method for Down-Regulation of
Amyloid
; FILE REFERENCE: 674542-2008
; CURRENT APPLICATION NUMBER: US/10/223,809A
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/337,543
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/373,027
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: DE 2001 01231
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: DE 2002 0058
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-223-809A-4

Query Match 100.0%; Score 74; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 10

US-10-261-446-19

; Sequence 19, Application US/10261446

; Publication No. US20030165526A1

; GENERAL INFORMATION:

; APPLICANT: Kuzyk, Michael A.

; APPLICANT: Burian, Jan

; APPLICANT: Kay, William W.

; APPLICANT: Thornton, Julian C.

; TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST

; TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE

THERAPY

; FILE REFERENCE: 4616-64094

; CURRENT APPLICATION NUMBER: US/10/261,446

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US 09/677,374

; PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/154,437

; PRIOR FILING DATE: 1999-09-17

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 19

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Clostridium tetani

US-10-261-446-19

Query Match 100.0%; Score 74; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 8e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15

|||||

Db 1 QYIKANSKFIGITEL 15

RESULT 11

US-10-239-313A-618

; Sequence 618, Application US/10239313A

; Publication No. US20030175285A1

; GENERAL INFORMATION:

; APPLICANT: KLINGUER - HAMOUR, Christine

; APPLICANT: CORVAIA, Nathalie

; APPLICANT: BECK, Alain

; APPLICANT: GOETSCH, Liliane

; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS

; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM

; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

; FILE REFERENCE: 343 727 - US

; CURRENT APPLICATION NUMBER: US/10/239,313A

; CURRENT FILING DATE: 2002-09-19

; PRIOR APPLICATION NUMBER: FR 00/03711

; PRIOR FILING DATE: 2000-03-23

; PRIOR APPLICATION NUMBER: PCT 01/70772

; PRIOR FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 618
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-239-313A-618

Query Match 100.0%; Score 74; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
|||||||
Db 1 QYIKANSKFIGITEL 15

RESULT 12

US-10-295-074-3

; Sequence 3, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Tetanus toxoid P2 epitope
US-10-295-074-3

Query Match 100.0%; Score 74; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
|||||||
Db 1 QYIKANSKFIGITEL 15

RESULT 13

US-10-372-111-7

; Sequence 7, Application US/10372111
; Publication No. US20040009169A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Julie
; APPLICANT: Yednock, Ted A.
; TITLE OF INVENTION: Administration of Agents for the Treatment of
Inflammation
; FILE REFERENCE: 002010-798
; CURRENT APPLICATION NUMBER: US/10/372,111

; CURRENT FILING DATE: 2003-05-25
; PRIOR APPLICATION NUMBER: US 60/374,501
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/360,134
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Tetanus toxoid
US-10-372-111-7

Query Match 100.0%; Score 74; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 14

US-10-261-445B-19

; Sequence 19, Application US/10261445B
; Publication No. US20040086524A1
; GENERAL INFORMATION:
; APPLICANT: Kuzyk, Michael A.
; APPLICANT: Burian, Jan
; APPLICANT: Kay, William W.
; APPLICANT: Thornton, Julian C.
; TITLE OF INVENTION: VACCINES AND AGENTS FOR INDUCING IMMUNITY IN FISH AGAINST
; TITLE OF INVENTION: RICKETTSIAL DISEASES, AND ASSOCIATED PREVENTATIVE
THERAPY
; FILE REFERENCE: 4616-64095
; CURRENT APPLICATION NUMBER: US/10/261,445B
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 09/677,374
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/154,437
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-261-445B-19

Query Match 100.0%; Score 74; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
| | | | | | | | | | | | | | |
Db 1 QYIKANSKFIGITEL 15

RESULT 15
 US-10-664-801-34
 ; Sequence 34, Application US/10664801
 ; Publication No. US20040115199A1
 ; GENERAL INFORMATION:
 ; APPLICANT: M&E Biotech A/S
 ; APPLICANT: HALKIER, Torben
 ; APPLICANT: HAANING, Jesper
 ; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
 ; TITLE OF INVENTION: Activity
 ; FILE REFERENCE: 22021 PC 1
 ; CURRENT APPLICATION NUMBER: US/10/664,801
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: US/09/396,937
 ; PRIOR FILING DATE: 1999-09-15
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 34
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Clostridium tetani
 US-10-664-801-34

Query Match 100.0%; Score 74; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 1 QYIKANSKFIGITEL 15

Search completed: August 13, 2004, 09:33:24
 Job time : 3.82051 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:53 ; Search time 2.28938 Seconds
(without alignments)
2067.275 Million cell updates/sec

Title: US-09-785-215-4
Perfect score: 74
Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Query	Length	DB	ID	Description
No.							

1	74	100.0	1310	2	Q93N27	Q93n27 clostridium
2	46	62.2	447	16	Q7VQH3	Q7vqh3 candidatus
3	46	62.2	880	16	Q835J8	Q835j8 enterococcu
4	44.5	60.1	60	7	Q31585	Q31585 salmo salar
5	44.5	60.1	71	7	Q9XRJ9	Q9xrx9 salvelinus
6	44.5	60.1	85	7	Q95IS2	Q95is2 salmo salar
7	44.5	60.1	85	7	Q95HY1	Q95hyl1 salmo salar
8	44.5	60.1	86	7	Q95HX4	Q95hx4 salmo salar
9	44.5	60.1	244	7	Q31590	Q31590 salmo salar
10	44	59.5	546	10	Q9XG37	Q9xg37 guillardia
11	43.5	58.8	67	7	Q31578	Q31578 salmo salar
12	43	58.1	180	16	Q9CF66	Q9cf66 lactococcus
13	43	58.1	250	9	Q9MCL7	Q9mcl7 streptococc
14	43	58.1	252	9	Q9XJE8	Q9xje8 lactococcus
15	43	58.1	291	11	Q9CRV4	Q9crv4 mus musculu
16	43	58.1	304	11	Q8K2A1	Q8k2a1 mus musculu
17	43	58.1	309	11	Q9CYD2	Q9cyd2 mus musculu
18	43	58.1	572	10	Q8H8F3	Q8h8f3 oryza sativ
19	43	58.1	899	12	Q9YTK4	Q9ytk4 ateline her
20	42.5	57.4	1087	5	Q25961	Q25961 plasmodium
21	42.5	57.4	1694	5	Q9NHX1	Q9nhx1 plasmodium
22	42.5	57.4	1694	5	Q9Tzt5	Q9tzt5 plasmodium
23	42.5	57.4	1704	5	Q9Tzt4	Q9tzt4 plasmodium
24	42.5	57.4	1720	5	Q25922	Q25922 plasmodium
25	42.5	57.4	1720	5	Q8IOU8	Q8iou8 plasmodium
26	42	56.8	358	17	Q8TZU8	Q8tzu8 pyrococcus
27	42	56.8	455	2	Q84F64	Q84f64 photorhabdu
28	42	56.8	1333	5	Q24262	Q24262 drosophila
29	41.5	56.1	84	13	Q9DEK4	Q9dek4 coregonus s
30	41.5	56.1	85	7	Q95IS3	Q95is3 salmo salar
31	41.5	56.1	85	7	Q95IR2	Q95ir2 salmo salar
32	41.5	56.1	149	7	Q31495	Q31495 oncorhynchu
33	41.5	56.1	216	7	Q9GJH0	Q9gjh0 salmo trutt
34	41.5	56.1	216	7	Q9GJG9	Q9gjj9 salmo trutt
35	41	55.4	187	16	Q8R9Q7	Q8r9q7 thermoanaer
36	41	55.4	208	16	Q831B2	Q831b2 enterococcu
37	41	55.4	247	11	Q9D3B9	Q9d3b9 mus musculu
38	41	55.4	384	4	Q9HD07	Q9hd07 homo sapien
39	41	55.4	447	16	Q97HK7	Q97hk7 clostridium
40	41	55.4	532	5	O96671	O96671 drosophila
41	41	55.4	532	5	Q9VU53	Q9vu53 drosophila
42	41	55.4	595	11	Q8CAD2	Q8cad2 mus musculu
43	41	55.4	626	11	Q8BRL1	Q8brl1 mus musculu
44	41	55.4	689	5	Q8IHZ2	Q8ihz2 plasmodium
45	41	55.4	749	4	Q8NEI0	Q8nei0 homo sapien

ALIGNMENTS

RESULT 1

Q93N27

ID Q93N27 PRELIMINARY; PRT; 1310 AA.
AC Q93N27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Tetanus toxin (Fragment).
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shumin Z., Dianliang L.;
 RT "Cloning and sequence analysis of tetanus toxin gene."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF389424; AAK72964.2; -.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 FT NON_TER 1 1
 FT NON_TER 1310 1310
 SQ SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 1310;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 |||||
 Db 831 QYIKANSKFIGITEL 845

RESULT 2

Q7VQH3

ID Q7VQH3 PRELIMINARY; PRT; 447 AA.
 AC Q7VQH3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Enolase (EC 4.2.1.11).
 GN ENO OR BFL157.
 OS Candidatus Blochmannia floridanus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
 OX NCBI_TaxID=203907;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22784745; PubMed=12886019;
 RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,

RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
 RA van Ham R.C.H.J., Gross R., Moya A.;
 RT "The genome sequence of *Blochmannia floridanus*: comparative analysis
 RT of reduced genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
 DR EMBL; BX248584; CAD83678.1; -.
 KW Lyase; Complete proteome.
 SQ SEQUENCE 447 AA; 49005 MW; 465B69C3273C7AC4 CRC64;

Query Match 62.2%; Score 46; DB 16; Length 447;
 Best Local Similarity 46.7%; Pred. No. 9.2;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 ::| ||| |:|:
 Db 416 EFLKDNSKFYGVNEI 430

RESULT 3

Q835J8

ID Q835J8 PRELIMINARY; PRT; 880 AA.
 AC Q835J8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Alanyl-tRNA synthetase.
 GN ALAS OR EF1379.
 OS *Enterococcus faecalis* (*Streptococcus faecalis*).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT *Enterococcus faecalis*.";
 RL Science 299:2071-2074(2003).
 DR EMBL; AE016951; AAO81170.1; -.
 DR TIGR; EF1379; -.
 DR GO; GO:0004813; F:alanine-tRNA ligase activity; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0006419; P:alanyl-tRNA aminoacylation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR003156; DHHA1.
 DR InterPro; IPR000169; SHprot_acsite.
 DR InterPro; IPR002318; tRNA-synt_2c.
 DR InterPro; IPR006193; tRNA_synt_Ala.
 DR Pfam; PF02272; DHHA1; 1.
 DR Pfam; PF01411; tRNA-synt_2c; 1.

DR PRINTS; PR00980; TRNASYNTHALA.
 DR TIGRFAMs; TIGR00344; alaS; 1.
 DR PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
 KW Aminoacyl-tRNA synthetase; Complete proteome.
 SQ SEQUENCE 880 AA; 97887 MW; EF23ED1229B6683F CRC64;

Query Match 62.2%; Score 46; DB 16; Length 880;
 Best Local Similarity 69.2%; Pred. No. 18;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 IKANSKFIGITEL 15
 || |||:| |||
 Db 455 IKVESKFVGYTEL 467

RESULT 4

Q31585

ID Q31585 PRELIMINARY; PRT; 60 AA.
 AC Q31585;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE (DB02) MHC class II beta 1 (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
 RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
 RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
 RL Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L24953; AAA49597.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 60 60
 SQ SEQUENCE 60 AA; 6776 MW; 5D4F3449060940E2 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 60;
 Best Local Similarity 55.6%; Pred. No. 2.4;
 Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
 :||: || ||:| |||
 Db 16 EYIRFNSTVGKFVGYTEL 33

RESULT 5

Q9XRJ9

ID Q9XRJ9 PRELIMINARY; PRT; 71 AA.
AC Q9XRJ9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II beta 1 (Fragment).
GN SANA.
OS Salvelinus namaycush (lake trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8040;
RN [1]
RP SEQUENCE FROM N.A.
RA Dorschner M.O., Duris T., Phillips R.B.;
RT "Diversity of a Lake Trout Mhc class II Gene."
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF130026; AAD20889.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8002 MW; E3095286582A9F2D CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 71;
Best Local Similarity 55.6%; Pred. No. 2,8;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
:|: || |:| |||
Db 14 EYIRENSTVGKFGVGYTEL 31

RESULT 6

Q95IS2

ID Q95IS2 PRELIMINARY; PRT; 85 AA.
AC Q95IS2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II beta chain (Fragment).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]

RP SEQUENCE FROM N.A.
 RA Landry C., Bernatchez L.;
 RT "Comparative analysis of population structure across environments and
 RT geographic scales at Major Histocompatibility Complex and
 RT microsatellite in Atlantic salmon (*Salmo salar*).";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF373699; AAK61882.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 85 85
 SQ SEQUENCE 85 AA; 9743 MW; 3214E01AD1B66AC5 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 85;
 Best Local Similarity 55.6%; Pred. No. 3.3;
 Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
 :||: || ||:| |||
 Db 33 EYIRENSTVGKFGVGYTEL 50

RESULT 7

Q95HY1

ID Q95HY1 PRELIMINARY; PRT; 85 AA.
 AC Q95HY1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MHC class II B antigen (Fragment).
 GN DB1.
 OS *Salmo salar* (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; *Salmo*.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383619; PubMed=11491536;
 RA Langefors A., Lohm J., von Schantz T.;
 RT "Allelic polymorphism in MHC class II B in four populations of
 RT Atlantic salmon (*Salmo salar*).";
 RL Immunogenetics 53:329-336(2001).
 DR EMBL; AF104370; AAL04002.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.

DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 85 85
SQ SEQUENCE 85 AA; 9723 MW; 27C9F7931F1F01C4 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 85;
Best Local Similarity 55.6%; Pred. No. 3.3;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
: ||: || ||: | |||
Db 33 EYIRFNSTVGKFGVGYTEL 50

RESULT 8

Q95HX4

ID Q95HX4 PRELIMINARY; PRT; 86 AA.
AC Q95HX4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II B antigen (Fragment).
GN DB1.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383619; PubMed=11491536;
RA Langefors A., Lohm J., von Schantz T.;
RT "Allelic polymorphism in MHC class II B in four populations of
RT Atlantic salmon (Salmo salar).";
RL Immunogenetics 53:329-336(2001).
DR EMBL; AF104377; AAL04009.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9912 MW; E5097729F681F149 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 86;
Best Local Similarity 55.6%; Pred. No. 3.4;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
: ||: || ||: | |||

Db 33 EYIRFNSTVGKFVGYTEL 50

RESULT 9

Q31590

ID Q31590 PRELIMINARY; PRT; 244 AA.
AC Q31590;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class II.
GN MHC-SASA CLASS II B.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=93170890; PubMed=8436418;
RA Hordvik I., Grimholt U., Fosse V.M., Lie Y., Endresen C.;
RT "Cloning and sequence analysis of cDNAs encoding the MHC class II a-
RT chain in Atlantic salmon, Salmo salar.";
RL Immunogenetics 37:437-441(1993).
DR EMBL; X70166; CAA49725.1; -.
DR PIR; S29982; S29982.
DR HSSP; P01888; 1BMG.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 244 AA; 27449 MW; 496CB9EA9D73765C CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 244;
Best Local Similarity 55.6%; Pred. No. 9.4;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
: ||: || ||: | ||
Db 51 EYIRFNSTVGKFVGYTEL 68

RESULT 10

Q9XG37

ID Q9XG37 PRELIMINARY; PRT; 546 AA.
AC Q9XG37;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Guillardia theta (Cryptomonas phi).
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
 OX NCBI_TaxID=55529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20087226; PubMed=10618395;
 RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
 RA Cavalier-Smith T., Maier U., Douglas S.;
 RT "Chloroplast protein and centrosomal genes, a tRNA intron, and odd
 RT telomeres in an unusually compact eukaryotic genome, the cryptomonad
 RT nucleomorph.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21223349; PubMed=11323671;
 RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.,
 RA Wu X., Reith M., Cavalier-Smith T., Maier U.;
 RT "The highly reduced genome of an enslaved algal nucleus.";
 RL Nature 410:1091-1096(2001).
 DR EMBL; AJ010592; CAB40403.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 546 AA; 66218 MW; 7303950F632BE6F2 CRC64;

Query Match 59.5%; Score 44; DB 10; Length 546;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YIKANSKFIGITEL 15
 :||:|:|:|: :||:
 Db 445 FIKSNSRFMRLTEI 458

RESULT 11

Q31578

ID Q31578 PRELIMINARY; PRT; 67 AA.
 AC Q31578;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE (DB03) MHC class II beta 1 (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
 RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
 RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
 RL Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; L24929; AAA49590.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 67 67
 SQ SEQUENCE 67 AA; 7449 MW; 42771AEDBABA6626 CRC64;

Query Match 58.8%; Score 43.5; DB 7; Length 67;
 Best Local Similarity 50.0%; Pred. No. 4;
 Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
 :|:: || ||:| |||
 Db 16 EYVRFNSTVGKFGVGYTEL 33

RESULT 12

Q9CF66

ID Q9CF66 PRELIMINARY; PRT; 180 AA.
 AC Q9CF66;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Spermidine acetyltransferase (EC 2.3.1.57).
 GN YQFF OR LL1615.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403."
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006391; AAK05713.1; -.
 DR PIR; G86826; G86826.
 DR GO; GO:0004145; F:diamine N-acetyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR000182; GCN5acetyl_trans.
 DR Pfam; PF00583; Acetyltransf; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 180 AA; 21022 MW; 6DBD148524C0DF3C CRC64;

Query Match 58.1%; Score 43; DB 16; Length 180;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 IKANSKFIGITEL 15
 |:|| |||| ||

Db

65 IEANDTFIGIVEL 77

RESULT 13

Q9MCL7

ID Q9MCL7 PRELIMINARY; PRT; 250 AA.
AC Q9MCL7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF13.
GN ORF13.
OS Streptococcus thermophilus bacteriophage 7201.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=112023;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20088830; PubMed=10620678;
RA Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,
RA van Sinderen D.;
RT "Identification of four loci isolated from two Streptococcus
RT thermophilus phage genomes responsible for mediating bacteriophage
RT resistance.";
RL FEMS Microbiol. Lett. 182:271-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.;
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF145054; AAF43506.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR002295; D21N6_mtfase.
DR InterPro; IPR001091; Met_trans_CN4.
DR InterPro; IPR002941; N6/N4_Mtase.
DR Pfam; PF01555; N6_N4_Mtase; 1.
DR PRINTS; PR00506; D21N6MTFRASE.
DR PRINTS; PR00508; S21N4MTFRASE.
SQ SEQUENCE 250 AA; 28744 MW; 725EA3B2B56B0D7F CRC64;

Query Match 58.1%; Score 43; DB 9; Length 250;
Best Local Similarity 57.1%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITE 14
| :||| | :| ||
Db 131 QVLKANMKIVGATE 144

RESULT 14

Q9XJE8

ID Q9XJE8 PRELIMINARY; PRT; 252 AA.
AC Q9XJE8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methylase.

OS Lactococcus lactis bacteriophage Tuc2009.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=35241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F.;
 RT "Molecular analysis of the temperate lactococcal phage Tuc2009."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF109874; AAD37103.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
 DR GO; GO:0006306; P:DNA methylation; IEA.
 DR InterPro; IPR002295; D21N6_mtfrase.
 DR InterPro; IPR001091; Met_trans_CN4.
 DR InterPro; IPR002941; N6/N4_Mtase.
 DR Pfam; PF01555; N6_N4_Mtase; 1.
 DR PRINTS; PR00506; D21N6MTFRASE.
 DR PRINTS; PR00508; S21N4MTFRASE.
 KW Methyltransferase.
 SQ SEQUENCE 252 AA; 29357 MW; 4D5A59FF47363948 CRC64;

Query Match 58.1%; Score 43; DB 9; Length 252;
 Best Local Similarity 57.1%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITE 14
 | :||| | :| ||
 Db 130 QVLKANMKIVGATE 143

RESULT 15

Q9CRV4

ID Q9CRV4 PRELIMINARY; PRT; 291 AA.
 AC Q9CRV4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 13 days embryo head cDNA, RIKEN full-length enriched library,
 DE clone:3110030A04 product:CED-6 protein homolog.
 GN CED6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 DR EMBL; AK014093; BAB29151.2; -.
 DR MGD; MGI:1920407; Ced6.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR006020; PTB_PID.
 DR Pfam; PF00640; PID; 1.
 DR SMART; SM00462; PTB; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.

DR PROSITE; PS01179; PID; 1.

SQ SEQUENCE 291 AA; 32802 MW; 91FF3F41CD0BC6F2 CRC64;

Query Match 58.1%; Score 43; DB 11; Length 291;

Best Local Similarity 57.1%; Pred. No. 21;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YIKANSKFIGITEL 15

|| |:|:|:| ||:

Db 11 YIPYNAKFLGSTEV 24

Search completed: August 13, 2004, 09:15:36

Job time : 4.28938 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:28 ; Search time 0.549451 Seconds
 (without alignments)
 1421.515 Million cell updates/sec

Title: US-09-785-215-4
 Perfect score: 74
 Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result.		Query						
No.	Score	Match	Length	DB	ID		Description	
<hr/>								
1	74	100.0	1314	1	TETX_CLOTE	P04958	clostridium	
2	44	59.5	66	1	VG84_BPML5	Q05301	mycobacteri	
3	42.5	57.4	1682	1	MSP1_PLAF3	P19598	plasmodium	
4	42.5	57.4	1701	1	MSP1_PLAFF	P13819	plasmodium	
5	42.5	57.4	1701	1	MSP1_PLAFM	P08569	plasmodium	
6	42.5	57.4	1726	1	MSP1_PLAFC	P04934	plasmodium	
7	42.5	57.4	1726	1	MSP1_PLAFP	P50495	plasmodium	
8	41	55.4	204	1	PYRC_SERMA	Q9s3s1	serratia ma	
9	41	55.4	384	1	LE12_THETN	Q8rcf9	thermoanaer	
10	41	55.4	899	1	V120_HSVSA	Q01055	herpesvirus	
11	40	54.1	194	1	ACPD_HAEIN	P43013	haemophilus	
12	40	54.1	601	1	PEF1_LACLC	P54124	lactococcus	
13	40	54.1	601	1	PEPF_LACLA	Q9cev7	lactococcus	
14	40	54.1	644	1	YHJ9_YEAST	P38694	saccharomyc	
15	39	52.7	213	1	KAD_MYCCA	P10251	mycoplasma	
16	39	52.7	505	1	GPMI_MYCPU	Q98qa7	mycoplasma	
17	38	51.4	256	1	YD83_METJA	Q58778	methanococc	

18	38	51.4	287	1	TRUB_AQUAE	O66922	aquifex aeo
19	38	51.4	572	1	HEMA_PI3HT	P12562	human parai
20	37	50.0	191	1	Y096_HAEIN	P43940	haemophilus
21	37	50.0	195	1	ACPD_VIBVU	Q8da68	vibrio vuln
22	37	50.0	231	1	PYRF_MYCPE	Q8euy3	mycoplasma
23	37	50.0	445	1	GNT1_HUMAN	P26572	homo sapien
24	37	50.0	447	1	GNT1_MOUSE	P27808	mus musculu
25	37	50.0	447	1	GNT1_RABIT	P27115	oryctolagus
26	37	50.0	447	1	GNT1_RAT	Q09325	rattus norv
27	37	50.0	490	1	Y032_BORBU	O51063	borrelia bu
28	37	50.0	510	1	G6PD_ASPNG	P48826	aspergillus
29	37	50.0	511	1	G6PD_EMENI	P41764	emericella
30	37	50.0	548	1	2AD1_SCHPO	Q10428	schizosacch
31	36	48.6	169	1	Y358_BUCAI	P57439	buchnera ap
32	36	48.6	258	1	MIP_CHLPN	Q9z7p3	chlamydia p
33	36	48.6	296	1	YD01_CLOAB	P33659	clostridium
34	36	48.6	333	1	DPOB_XENLA	O57383	xenopus lae
35	36	48.6	451	1	MURD_BACSU	Q03522	bacillus su
36	36	48.6	461	1	NIFN_RHOCA	P19077	rhodobacter
37	36	48.6	495	1	G6PD_PICJA	P11410	pichia jadi
38	36	48.6	627	1	2AD2_SCHPO	P78759	schizosacch
39	36	48.6	630	1	YND1_YEAST	P40009	saccharomyc
40	36	48.6	774	1	RRP3_INCBE	P21770	influenza c
41	36	48.6	774	1	RRP3_INCJJ	P13877	influenza c
42	36	48.6	1630	1	MSP1_PLAFK	P04932	plasmodium
43	36	48.6	1639	1	MSP1_PLAFW	P04933	plasmodium
44	35	47.3	176	1	NU6C_SPIOL	Q9m3i8	spinacia ol
45	35	47.3	200	1	ACD2_CLOAB	Q97dq1	clostridium

ALIGNMENTS

RESULT 1

TETX_CLOTE

ID TETX_CLOTE STANDARD; PRT; 1314 AA.
AC P04958;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylisin) [Contains:
DE Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
DE chain (Tetanus toxin chain H)].
GN TETX OR CTP60.
OS Clostridium tetani.
OG Plasmid pE88, and Plasmid 75 Kbp.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=87053814; PubMed=3536478;
RA Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,
RA Weller U., Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in E. coli, and
RT homology with botulinum toxins.";

RL EMBO J. 5:2495-2502(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CN3911; PLASMID=75 Kbp;
 RX MEDLINE=87040747; PubMed=3774547;
 RA Fairweather N.F., Lyness V.A.;
 RT "The complete nucleotide sequence of tetanus toxin.";
 RL Nucleic Acids Res. 14:7809-7812(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Massachusetts / E88; PLASMID=pE88;
 RX MEDLINE=22457253; PubMed=12552129;
 RA Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 RT tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
 RN [4]
 RP SEQUENCE OF 742-1314 FROM N.A.
 RC PLASMID=75 Kbp;
 RX MEDLINE=86085672; PubMed=3510187;
 RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
 RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
 RT fragment C in Escherichia coli.";
 RL J. Bacteriol. 165:21-27(1986).
 RN [5]
 RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=90201034; PubMed=2108021;
 RA Krieglstein K., Henschen A., Weller U., Habermann E.;
 RT "Arrangement of disulfide bridges and positions of sulfhydryl groups
 RT in tetanus toxin.";
 RL Eur. J. Biochem. 188:39-45(1990).
 RN [6]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=92037649; PubMed=1935979;
 RA Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;
 RT "Limited proteolysis of tetanus toxin. Relation to activity and
 RT identification of cleavage sites.";
 RL Eur. J. Biochem. 202:41-51(1991).
 RN [7]
 RP IDENTIFICATION AS ZINC-PROTEASE.
 RX MEDLINE=93010948; PubMed=1396558;
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RA Montecucco C.;
 RT "Tetanus toxin is a zinc protein and its inhibition of
 RT neurotransmitter release and protease activity depend on zinc.";
 RL EMBO J. 11:3577-3583(1992).
 RN [8]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93063293; PubMed=1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 RT by proteolytic cleavage of synaptobrevin.";
 RL Nature 359:832-835(1992).
 RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
 RX MEDLINE=97475217; PubMed=9334741;
 RA Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 RT neurotoxin.";
 RL Nat. Struct. Biol. 4:788-792(1997).
 CC -!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
 CC BOND OF SYNAPTOSOMALIN-2.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
 CC synaptosomalin 2.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 CC YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 CC AND ARE NON-TOXIC AFTER SEPARATION.
 CC -!- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 CC GANGLIOSIDE RECEPTORS.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X04436; CAA28033.1; -.
 DR EMBL; X06214; CAA29564.1; -.
 DR EMBL; AF528097; AA037454.1; -.
 DR EMBL; M12739; AAA23282.1; -.
 DR PIR; A25689; BTCLTN.
 DR PDB; 1AF9; 29-APR-98.
 DR PDB; 1A8D; 14-OCT-98.
 DR PDB; 1D0H; 27-MAR-00.
 DR PDB; 1DFQ; 24-MAR-00.
 DR PDB; 1DIW; 24-MAR-00.
 DR PDB; 1DLL; 24-MAR-00.
 DR PDB; 1FV3; 05-SEP-01.
 DR MEROPS; M27.001; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOLILYSIN.
 DR ProDom; PD001963; Bontolilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 KW 3D-structure; Complete proteome.
 FT INIT_MET 0 0
 FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.

FT	CHAIN	457	1314
FT	METAL	232	232
FT	ACT_SITE	233	233
FT	METAL	236	236
FT	TRANSMEM	226	246
FT	TRANSMEM	669	689
FT	DISULFID	438	466
FT	DISULFID	1076	1092
FT	HELIX	876	882
FT	TURN	883	883
FT	STRAND	884	891
FT	TURN	892	893
FT	STRAND	894	897
FT	STRAND	904	907
FT	TURN	909	910
FT	STRAND	912	915
FT	STRAND	920	925
FT	TURN	928	929
FT	STRAND	932	935
FT	HELIX	938	940
FT	TURN	941	946
FT	STRAND	949	956
FT	HELIX	962	968
FT	TURN	969	970
FT	STRAND	972	977
FT	STRAND	980	981
FT	HELIX	983	985
FT	STRAND	987	995
FT	TURN	996	997
FT	STRAND	998	1004
FT	TURN	1006	1007
FT	STRAND	1010	1016
FT	STRAND	1020	1020
FT	TURN	1021	1022
FT	STRAND	1031	1037
FT	TURN	1039	1040
FT	STRAND	1042	1047
FT	TURN	1048	1049
FT	STRAND	1050	1056
FT	TURN	1058	1059
FT	STRAND	1068	1074
FT	TURN	1079	1080
FT	STRAND	1082	1091
FT	HELIX	1097	1105
FT	TURN	1106	1107
FT	STRAND	1112	1112
FT	STRAND	1114	1114
FT	TURN	1116	1117
FT	STRAND	1120	1120
FT	STRAND	1122	1122
FT	TURN	1123	1124
FT	STRAND	1127	1131
FT	HELIX	1132	1134
FT	TURN	1135	1136
FT	STRAND	1137	1141
FT	TURN	1144	1145
FT	STRAND	1148	1152

TETANUS TOXIN HEAVY CHAIN.
 ZINC (CATALYTIC) (BY SIMILARITY).
 BY SIMILARITY.
 ZINC (CATALYTIC) (BY SIMILARITY).
 POTENTIAL.
 POTENTIAL.
 INTERCHAIN.

```

FT   STRAND      1155   1158
FT   TURN        1159   1162
FT   STRAND      1163   1166
FT   STRAND      1173   1178
FT   TURN        1184   1185
FT   STRAND      1188   1188
FT   STRAND      1190   1190

```

```

Query Match          100.0%;  Score 74;  DB 1;  Length 1314;
Best Local Similarity 100.0%;  Pred. No. 2e-05;
Matches    15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy          1 QYIKANSKFIGITEL 15
            |||||
Db          829 QYIKANSKFIGITEL 843

```

RESULT 2

VG84_BPML5

```

ID   VG84_BPML5      STANDARD;          PRT;          66 AA.
AC   Q05301;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   Gene 84 protein (GP84).
GN   84.
OS   Mycobacteriophage L5.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC   L5-like viruses.
OX   NCBI_TaxID=31757;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93211282; PubMed=8459766;
RA   Hatfull G.F., Sarkis G.J.;
RT   "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT   a phage system for mycobacterial genetics.";
RL   Mol. Microbiol. 7:395-405(1993).
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; Z18946; CAA79460.1; -.
DR   PIR; S31029; S31029.
SQ   SEQUENCE    66 AA;  7424 MW;  9C7104C7A4FA74A5 CRC64;

```

```

Query Match          59.5%;  Score 44;  DB 1;  Length 66;
Best Local Similarity 57.1%;  Pred. No. 0.32;
Matches     8;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

```

```

Qy          2 YIKANSKFIGITEL 15
            ||| | ||:| |:
Db          50 YIKRNGKFVGTWEV 63

```

RESULT 3

MSP1_PLAF3

ID MSP1_PLAF3 STANDARD; PRT; 1682 AA.
AC P19598; Q25921;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (PMMSA) (P190).
GN MSP-1.
OS Plasmodium falciparum (isolate ro-33 / Ghana).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5834;
RN [1]
RP SEQUENCE OF 1-1061 FROM N.A.
RX MEDLINE=88166657; PubMed=3327688;
RA Certa U., Rotmann D., Matile H., Reber-Liske R.;
RT "A naturally occurring gene encoding the major surface antigen
RT precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
RL EMBO J. 6:4137-4142(1987).
RN [2]
RP SEQUENCE OF 1032-1682 FROM N.A.
RX MEDLINE=95354793; PubMed=7628566;
RA Tolle R., Bujard H., Cooper J.A.;
RT "Plasmodium falciparum: variations within the C-terminal region of
RT merozoite surface antigen-1.";
RL Exp. Parasitol. 81:47-54(1995).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42
CC kDa and 19 kDa antigens which are the major surface antigens of
CC merozoites. The maturation take place during schizont.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M35727; AAA29715.1; -.
DR EMBL; Y00087; CAA68280.1; -.
DR EMBL; Z35326; CAA84555.1; -.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 1.
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
KW Transmembrane; GPI-anchor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1682 MEROZOITE SURFACE PROTEIN 1.
FT TRANSMEM 1666 1682 MEMBRANE ANCHOR (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 599 599 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	785	785	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	881	881	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	901	901	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	947	947	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1071	1071	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1178	1178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1569	1569	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1682 AA; 192462 MW; C82A1E159948CAD6 CRC64;		

Query Match 57.4%; Score 42.5; DB 1; Length 1682;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
 |::|:| | | | | | | |
 Db 983 QFVKSNSKVITGLTE 997

RESULT 4

MSP1_PLAFF

ID MSP1_PLAFF STANDARD; PRT; 1701 AA.
 AC P13819;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
 DE (PMMSA).
 GN MSP-1.
 OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88142999; PubMed=2449612;
 RA Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G.,
 RA Brown G.V., Anders R.F., Kemp D.J.;
 RT "Variation in the precursor to the major merozoite surface antigens
 RT of Plasmodium falciparum."
 RL Mol. Biochem. Parasitol. 27:291-302(1988).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42
 CC kDa and 19 kDa antigens which are the major surface antigens of
 CC merozoites. The maturation take place during schizont.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M19143; AAA29653.1; -.
 DR PIR; A54498; A54498.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 1.

KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
KW Transmembrane; GPI-anchor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1701 MEROZOITE SURFACE PROTEIN 1.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 470 470 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 802 802 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 899 899 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 919 919 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 965 965 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 991 991 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1588 1588 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1701 AA; 193719 MW; 3920B75E73D38552 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1701;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14
|::|:| | | |:
Db 1001 QFVKNSNSKVITGLTE 1015

RESULT 5

MSP1_PLAFM

ID MSP1_PLAFM STANDARD; PRT; 1701 AA.
AC P08569;
DT 01-AUG-1988 (Rel. 08, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (PMMSA) (P190).
GN MSP-1.
OS Plasmodium falciparum (isolate mad20 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=70153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88011243; PubMed=3079521;
RA Tanabe K., Mackay M., Goman M., Scaife J.G.;
RT "Allelic dimorphism in a surface antigen gene of the malaria parasite
RT Plasmodium falciparum."
RL J. Mol. Biol. 195:273-287(1987).
RN [2]
RP REVISIONS TO 1403; 1569 AND 1629.
RA Tanabe K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 1-115 FROM N.A.
RX MEDLINE=86136024; PubMed=3004972;
RA Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U.,
RA Stunnenberg H., Bujard H.;

RT "Polymorphism of the precursor for the major surface antigens of
RT Plasmodium falciparum merozoites: studies at the genetic level.";

RL EMBO J. 4:3823-3829(1985).

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).

CC -!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42
CC kDa and 19 kDa antigens which are the major surface antigens of
CC merozoites. The maturation take place during schizont.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X05624; CAA29112.1; -.

DR InterPro; IPR006209; EGF_like.

DR Pfam; PF00008; EGF; 1.

KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;

KW Transmembrane; GPI-anchor.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 1701 MEROZOITE SURFACE PROTEIN 1.

FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 470 470 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 536 536 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 802 802 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 899 899 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 919 919 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 965 965 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 991 991 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1588 1588 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 1701 AA; 193768 MW; 3FC2EC59AF96EA98 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1701;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:| | | | | | | |
Db 1001 QFVKSNSKVITGLTE 1015

RESULT 6

MSP1_PLAFC

ID MSP1_PLAFC STANDARD; PRT; 1726 AA.

AC P04934;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Merozoite surface protein 1 precursor (Merozoite surface antigens)

DE (PMMSA) (P195).

GN MSP-1.
 OS Plasmodium falciparum (isolate Camp / Malaysia).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5835;
 RN [1]
 RP SEQUENCE OF 1-1103 FROM N.A.
 RX MEDLINE=86205236; PubMed=3517809;
 RA Weber J.L., Leininger W.M., Lyon J.A.;
 RT "Variation in the gene encoding a major merozoite surface antigen of
 RT the human malaria parasite Plasmodium falciparum.";
 RL Nucleic Acids Res. 14:3311-3323(1986).
 RN [2]
 RP SEQUENCE OF 1104-1726 FROM N.A.
 RX MEDLINE=88143999; PubMed=3278296;
 RA Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
 RT "Merozoite surface protein sequence from the Camp strain of the human
 RT malaria parasite Plasmodium falciparum.";
 RL Nucleic Acids Res. 16:1206-1206(1988).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42
 CC kDa and 19 kDa antigens which are the major surface antigens of
 CC merozoites. The maturation take place during schizont.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X03831; CAA27446.1; -.
 DR PIR; A23386; SAZQGM.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 1.
 KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
 KW Transmembrane; GPI-anchor.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 1726 MEROZOITE SURFACE PROTEIN 1.
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 827 827 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 924 924 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 944 944 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 990 990 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1114 1114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1726 AA; 196197 MW; DD8AD45FA352BCF3 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1726;
 Best Local Similarity 60.0%; Pred. No. 16;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
|::|:| | | |:
Db 1026 QFVKSNSKVITGLTE 1040

RESULT 7

MSP1_PLAFP

ID MSP1_PLAFP STANDARD; PRT; 1726 AA.
AC P50495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (PMMSA) (GP195).
GN MSP-1.
OS Plasmodium falciparum (isolate Palo Alto / Uganda).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=57270;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89005525; PubMed=3049134;
RA Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
RA Siddiqui W.A.;
RT "Plasmodium falciparum: gene structure and hydropathy profile of the
RT major merozoite surface antigen (gp195) of the Uganda-Palo Alto
RT isolate.";
RL Exp. Parasitol. 67:1-11(1988).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42
CC kDa and 19 kDa antigens which are the major surface antigens of
CC merozoites. The maturation take place during schizont.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M37213; AAA29611.1; -.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 1.
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
KW Transmembrane; GPI-anchor.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1726 MEROZOITE SURFACE PROTEIN 1.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 567 567 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 827 827 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 924 924 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 944 944 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 990 990 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1016 1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1114 1114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1613 1613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1726 AA; 196174 MW; 5B59CEEFA2F9A026 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1726;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 QYIKANSKFI-GITE 14
 |::|:| | | | |
 Db 1026 QFVKSNSKVITGLTE 1040

RESULT 8

PYRC_SERMA

ID PYRC_SERMA STANDARD; PRT; 204 AA.
 AC Q9S3S1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Dihydroorotase (EC 3.5.2.3) (DHOase) (Fragment).
 GN PYRC.
 OS *Serratia marcescens*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Serratia*.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SM6;
 RA Berkmen M., Benedik M.J.;
 RT "DinI inhibits transcription of *Serratia marcescens* nuclease.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-
 CC aspartate.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
 CC -!- PATHWAY: Pyrimidine biosynthesis; third step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to the DHOase family. Subfamily 1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF175466; AAD50307.1; ALT_INIT.
 DR HAMAP; MF_00219; -; 1.
 DR InterPro; IPR006680; Amidohydro_1.
 DR InterPro; IPR002195; Pept_M38_nph.
 DR Pfam; PF01979; Amidohydro_1; 1.
 DR PROSITE; PS00482; DIHYDROOROTASE_1; PARTIAL.

DR PROSITE; PS00483; DIHYDROOROTASE_2; 1.
 KW Pyrimidine biosynthesis; Hydrolase; Metal-binding; Zinc.
 FT NON_TER 1 1
 FT METAL 34 34 ZINC 2 (BY SIMILARITY).
 FT METAL 107 107 ZINC 1 (BY SIMILARITY).
 SQ SEQUENCE 204 AA; 22899 MW; 9DB0B6C9B834B310 CRC64;

Query Match 55.4%; Score 41; DB 1; Length 204;
 Best Local Similarity 46.2%; Pred. No. 3.5;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGIT 13
 ||::| ::|:| |
 Db 42 QYVQAGNRFLGAT 54

RESULT 9

LE12_THETN

ID LE12_THETN STANDARD; PRT; 384 AA.
 AC Q8RCF9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 2-isopropylmalate synthase 2 (EC 2.3.3.13) (Alpha-isopropylmalate
 DE synthase 2) (Alpha-IPM synthetase 2).
 GN LEUA2 OR TTE0472.
 OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 11007;
 RX MEDLINE=21992816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;
 RT "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 CC -!- FUNCTION: Catalyzes the condensation of the acetyl group of
 CC acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form
 CC 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O =
 CC 2-hydroxy-2-isopropylsuccinate + CoA.
 CC -!- PATHWAY: Leucine biosynthesis; first step.
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate
 CC synthase family. LeuA 1 subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AE013018; AAM23753.1; -.
 DR HAMAP; MF_01025; atypical; 1.
 DR InterPro; IPR002034; AIPM/Hcit_synth.
 DR InterPro; IPR000891; HMGL-like.
 DR Pfam; PF00682; HMGL-like; 1.
 DR PROSITE; PS00815; AIPM_HOMOCIT_SYNTH_1; 1.
 DR PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
 KW Leucine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 384 AA; 42404 MW; 095310F2C0E4A4DD CRC64;

Query Match 55.4%; Score 41; DB 1; Length 384;
 Best Local Similarity 54.5%; Pred. No. 6.5;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IKANSKFIGIT 13
 :|| :||:|:|
 Db 214 VKAGAKFVGVT 224

RESULT 10

V120_HSVSA

ID V120_HSVSA STANDARD; PRT; 899 AA.
 AC Q01055;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Capsid assembly protein 63.
 GN 63 OR EERF1.
 OS Herpesvirus saimiri (strain 11).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=10383;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92333688; PubMed=1321287;
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
 RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
 RA Honess R.W.;
 RT "Primary structure of the herpesvirus saimiri genome.";
 RL J. Virol. 66:5047-5058(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92230228; PubMed=1314457;
 RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
 RT "Analysis of nucleotide sequence of the rightmost 43 kbp of
 RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
 RT organization between HVS and Epstein-Barr virus.";
 RL Virology 188:296-310(1992).
 CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
 CC EHV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCMV UL47.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL; X64346; CAA45686.1; -.

DR EMBL; M86409; AAA46139.1; -.

DR InterPro; IPR008643; Herpes_ORF63.

DR Pfam; PF05765; Herpes_ORF63; 1.

KW Capsid assembly.

SQ SEQUENCE 899 AA; 103350 MW; F1429B3770A2885E CRC64;

Query Match 55.4%; Score 41; DB 1; Length 899;

Best Local Similarity 50.0%; Pred. No. 15;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITE 14

||| :|: | |::|

Db 124 QYITSNATFTGLSE 137

RESULT 11

ACPD_HAEIN

ID ACPD_HAEIN STANDARD; PRT; 194 AA.

AC P43013;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Probable acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP phosphodiesterase).

GN ACPD OR HI1366.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OX NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=96186898; PubMed=8635745;

RA Chandler M.S., Smith R.A.;

RT "Characterization of the Haemophilus influenzae topA locus: DNA

topoisomerase I is required for genetic competence.";

RL Gene 169:25-31(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

RT "Whole-genome random sequencing and assembly of Haemophilus influenzae

Rd.";

RL Science 269:496-512(1995).

CC -!- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of

CC the phosphopantetheine prosthetic group from ACP (By similarity).
 CC -!- CATALYTIC ACTIVITY: Holo-[acyl-carrier protein] + H(2)O = 4'-
 CC phosphopantetheine + apo-[acyl-carrier protein].
 CC -!- SIMILARITY: Belongs to the acpD family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U20964; AAC43728.1; -.
 DR EMBL; U32816; AAC23013.1; -.
 DR PIR; G64026; G64026.
 DR TIGR; HI1366; -.
 DR HAMAP; MF_01216; -; 1.
 DR InterPro; IPR003680; NADHdh_2.
 DR Pfam; PF02525; Flavodoxin_2; 1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 194 AA; 21208 MW; A8AEC9D00829522C CRC64;

Query Match 54.1%; Score 40; DB 1; Length 194;
 Best Local Similarity 53.3%; Pred. No. 5;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
 ||:|: |||||::
 Db 147 QYMKSilGFIGITDV 161

RESULT 12

PEF1_LACLC

ID PEF1_LACLC STANDARD; PRT; 601 AA.
 AC P54124; P94880;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Oligoendopeptidase F, plasmid (EC 3.4.24.-).
 GN PEPF1 OR PEPF.
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OG Plasmid pLP763.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1359;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=NCDO 763;
 RX MEDLINE=95096044; PubMed=7798200;
 RA Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.;
 RT "Biochemical and genetic characterization of PepF, an oligopeptidase
 RT from Lactococcus lactis."
 RL J. Biol. Chem. 269:32070-32076(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCDO 763;
 RX MEDLINE=97352670; PubMed=9209029;

RA Nardi M., Renault P., Monnet V.;
 RT "Duplication of the pepF gene and shuffling of DNA fragments on the
 RT lactose plasmid of Lactococcus lactis.";
 RL J. Bacteriol. 179:4164-4171(1997).
 CC -!- FUNCTION: Hydrolyzes peptides containing between 7 and 17 amino
 CC acids with a rather wide specificity.
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M3.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z32522; CAA83534.1; -.
 DR EMBL; X99798; CAA68133.1; -.
 DR PIR; A55485; A55485.
 DR MEROPS; M03.007; -.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR001567; Peptidase_M3.
 DR InterPro; IPR004438; Peptidase_M3B.
 DR Pfam; PF01432; Peptidase_M3; 1.
 DR TIGRFAMs; TIGR00181; pepF; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW Hydrolase; Metalloprotease; Zinc; Plasmid.
 FT METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 388 388 BY SIMILARITY.
 FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CONFLICT 518 518 F -> S (IN REF. 2).
 SQ SEQUENCE 601 AA; 69674 MW; C8B5C519FFA2F787 CRC64;

Query Match 54.1%; Score 40; DB 1; Length 601;
 Best Local Similarity 46.7%; Pred. No. 16;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 :||: | :|||:
 Db 284 RYIELRKKILGITDL 298

RESULT 13

PEPF_LACLA

ID PEPF_LACLA STANDARD; PRT; 601 AA.
 AC Q9CEV7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Oligoendopeptidase F homolog (EC 3.4.24.-).
 GN PEPF OR LL1727.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
 RT *lactis* ssp. *lactis* IL1403.";
 RL Genome Res. 11:731-753(2001).
 CC -!- FUNCTION: Hydrolyzes peptides containing between 7 and 17 amino
 CC acids with a rather wide specificity (By similarity).
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M3.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE006403; AAK05825.1; -.
 DR PIR; G86840; G86840.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR001567; Peptidase_M3.
 DR InterPro; IPR004438; Peptidase_M3B.
 DR Pfam; PF01432; Peptidase_M3; 1.
 DR TIGRFAMs; TIGR00181; pepF; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Hydrolase; Metalloprotease; Zinc; Complete proteome.
 FT METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 388 388 BY SIMILARITY.
 FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 601 AA; 69883 MW; 045E6873F10FE19A CRC64;

Query Match 54.1%; Score 40; DB 1; Length 601;
 Best Local Similarity 46.7%; Pred. No. 16;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 :||: | :|||:|
 Db 284. RYIELRKKILGITDL 298

RESULT 14
 YHJ9_YEAST
 ID YHJ9_YEAST STANDARD; PRT; 644 AA.
 AC P38694;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical aldehyde-dehydrogenase like protein in FIL1-VMA10
 DE intergenic region (EC 1.2.1.-).
 GN YHR039C.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
 RT VIII.";
 RL Science 265:2077-2082(1994).
 CC -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00062; AAB68915.1; -.
 DR PIR; S46746; S46746.
 DR GermOnline; 139356; -.
 DR SGD; S0001081; MSC7.
 DR GO; GO:0007131; P:meiotic recombination; IMP.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Hypothetical protein; Oxidoreductase.
 FT ACT_SITE 354 354 BY SIMILARITY.
 FT ACT_SITE 389 389 BY SIMILARITY.
 SQ SEQUENCE 644 AA; 71320 MW; 54DADDAEB2A16D4D CRC64;

Query Match 54.1%; Score 40; DB 1; Length 644;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITEL 15
 | | : | | | | | |
 Db 38 QIIQDNQKLIGITT 52

RESULT 15

KAD_MYCCA

ID KAD_MYCCA STANDARD; PRT; 213 AA.
 AC P10251;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).

GN ADK.
 OS Mycoplasma capricolum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27343 / Kid;
 RX MEDLINE=88142549; PubMed=3481422;
 RA Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;
 RT "The ribosomal protein gene cluster of Mycoplasma capricolum."
 RL Mol. Gen. Genet. 210:314-322(1987).
 CC -!- FUNCTION: This small ubiquitous enzyme is essential for
 CC maintenance and cell growth.
 CC -!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the adenylate kinase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X06414; CAA29724.1; -.
 DR PIR; S02851; KIYMC.
 DR HSSP; P27142; 1ZIN.
 DR HAMAP; MF_00235; -; 1.
 DR InterPro; IPR006259; Adenyl_kin_sub.
 DR InterPro; IPR000850; Adenylate_kin.
 DR InterPro; IPR007862; ADK_lid.
 DR Pfam; PF00406; ADK; 1.
 DR Pfam; PF05191; ADK_lid; 1.
 DR PRINTS; PR00094; ADENYLTKNASE.
 DR ProDom; PD000657; Adenylate_kin; 1.
 DR TIGRFAMs; TIGR01351; adk; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; ATP-binding.
 FT NP_BIND 7 15 ATP (BY SIMILARITY).
 SQ SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;

Query Match 52.7%; Score 39; DB 1; Length 213;
 Best Local Similarity 72.7%; Pred. No. 8.4;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YIKANSKFIGI 12
 | | | | | | |
 Db 183 YFKTNSKFIEI 193

Search completed: August 13, 2004, 09:13:18
 Job time : 1.54945 secs